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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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10/609,078

06/27/2003

Edmund H. Crane III

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05/12/2005

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EXAMINER

KUBELIK, ANNE R

ART UNIT

PAPER NUMBER

1638

DATE MAILED: 05/12/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.		Applicant(s)	
	10/609,078		CRANE, EDMUND H.	
	Examiner		Art Unit	
	Anne R. Kubelik		1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☐ Responsive to communication(s) filed on ____.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-17 is/are pending in the application.
- 4a) Of the above claim(s) ____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) ____ is/are allowed.
- 6) ☒ Claim(s) 1-17 is/are rejected.
- 7) ☐ Claim(s) ____ is/are objected to.
- 8) ☐ Claim(s) ____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on ____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. ____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|---|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. ____. |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date ____. | 6) <input checked="" type="checkbox"/> Other: <u>search results</u> . |

DETAILED ACTION

1. Claims 1-17 are pending
2. In the IDS filed 27 June 2003 the BLAST alignment results have been crossed out, as these are not published literature. The information therein has been considered, however.

Claim Objections

3. Claims 1, 8-9 and 13 are objected to because of the following informalities:

Claim 1, part (g), has an improper article before the second "polynucleotide".

Claim 8 misspells "from".

Claims 9 and 13 have an improper article before "Rar-1" in part (a).

Claim Rejections - 35 USC § 112

4. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.
5. Claims 1-17 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claims contain subject matter that was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The claims are broadly drawn to nucleic acids that encode a maize protein that interacts with Rar1, that hybridize to SEQ ID NO: 2, 3, 7 or 9 under "high stringency conditions", that would be amplified from a maize nucleic acid library using primers that selectively hybridize

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under high stringency conditions to loci within SEQ ID NO: 2, 3, 7 or 9, that have 85% identity to SEQ ID NO:2, 3, 7 or 9, or that encode a protein with 85% identity to SEQ ID NO:8. The claims are also drawn to vectors and expression cassettes comprising the nucleic acids, cells and plants comprising the expression cassettes and methods of using the expression cassettes to modulate the level of Rar1-interactor protein in a plant and to enhance diseased resistance in a plant.

The instant specification, however, only provides guidance for yeast-two hybrid analysis to find maize nucleic acids encoding proteins that interact with the Rar1 protein (example 1), isolation of full-length cDNAs encoding the proteins (example 2); a BLAST comparison of the sequences of the nucleic acids (example 3); general guidance for transformation of maize, soybean and sunflower (examples 4-7). SEQ ID NO:1 encodes a protein that has homology to wheat heat-shock protein 80; SEQ ID NOs 2 and 3 are fragments of SEQ ID NO:7, which encodes a protein, SEQ ID NO:8, that has homology to rice SGT1; SEQ ID NO:9 is the coding sequence for that protein (pg 57).

The specification does not teach where to find or how to make nucleic acids that encode a maize protein that interacts with Rar1, that hybridize to SEQ ID NO: 2, 3, 7 or 9 under “high stringency conditions”, that would be amplified from a maize nucleic acid library using primers that selectively hybridize under high stringency conditions to loci within SEQ ID NO: 2, 3, 7 or 9, that have 85% identity to SEQ ID NO:2, 3, 7 or 9, or that encode a protein with 85% identity to SEQ ID NO:8.

Making substitutions in proteins does not produce predictable results. Hill et al (1998, Biochem. Biophys. Res. Comm. 244:573-577) teach that when three histidines that are

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maintained in ADP-glucose pyrophosphorylase across several species are substituted with the “nonconservative” amino acid glutamine, there is little effect on enzyme activity, while the substitution of one of those histidines with the “conservative” amino acid arginine drastically reduced enzyme activity (see Table 1).

Given the claim breath, unpredictability, and lack of guidance as discussed above, undue experimentation would have been required by one skilled in the art to develop and evaluate nucleic acids encoding proteins with 85% identity to SEQ ID NO:8. Making all possible single amino acid substitutions in an 361 protein like that of SEQ ID NO:8 would require making and analyzing 19^{361} nucleic acids; these proteins would have 99.7% identity to SEQ ID NO:8. Because nucleic acids encoding proteins with 85% identity to SEQ ID NO:1 would have 54 nucleotide substitutions, many more than 3^{691} nucleic acids would need to be made and analyzed. Guo et al. (2004, Proc. Natl. Acad. Sci. USA 101: 9205-9210) teach that while proteins are fairly tolerant to mutations resulting in single amino acid changes, increasing the number of substitutions additively increases the probability that the protein will be inactivated (pg 9209, right column, paragraph 2). Thus, making and analyzing proteins with 54 amino acid substitutions that also have Rar-1 interactor activity would require undue experimentation.

The specification does not teach how to use nucleic acids that encode a maize protein that interacts with Rar1, that hybridize to SEQ ID NO: 2, 3, 7 or 9 under “high stringency conditions”, that would be amplified from a maize nucleic acid library using primers that selectively hybridize under high stringency conditions to loci within SEQ ID NO: 2, 3, 7 or 9, that have 85% identity to SEQ ID NO:2, 3, 7 or 9, or that encode a protein with 85% identity to SEQ ID NO:8.

The specification teaches that the invention is a method of modulating the level of a protein and enhancing disease resistance in a plant by transformation with a nucleic acid of the invention (pg 3, lines 8-12; pg 4, lines 11-20); and that modulating the level of the protein can be accomplished by up or down regulation of the gene (pg 45, line 26, to pg 47, line 2). the specification does not teach which method, up-regulation or down-regulation will enhance disease resistance in a plant, and thus does not teach how to use the instant nucleic acid.

In *N. benthamiana* suppression of SGT1 resulted in plants that have lost resistance to tobacco rattle virus (Liu et al, July 2002, Plant Cell 14:1483-1496; see pg 1488, right column paragraph 4), and silencing of the barley SGT1 gene resulted in the reduction of R-gene-dependent disease resistance (Azevedo et al, pg 2075, column 3, paragraph 3). Thus, the claimed nucleic acid cannot be used in an antisense manner to enhance disease resistance in a plant, and SEQ ID NO:2 and 3, which are only partial sequences and can only be used in an antisense method cannot be used enhance disease resistance in a plant. Furthermore, a method of reducing the level of SGT1 protein in a plant has no use, given that plants without disease resistance have no utility.

The protein of SEQ ID NO:8 has 61.7% similarity to *Arabidopsis* SGT1a and 61.0% similarity to SGT1b (see sequence search results); it is not clear to which, if either, SEQ ID NO:8 is functionally equivalent. Austin et al (March, 2002, Science 295:2077-2080) teach that AtSGT1b is essential for resistance, while AtSGT1a is not (pg 2078, column 1, paragraphs 2-3), even though both interact with RAR1 in a yeast two-hybrid assay (Azevedo et al, March 2002, Science 295:2073-2076; see pg 2074, column 1, paragraph 3). AtSGT1a was also unable to

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complement *Nicotinana benthamiana* SGT1, while AtSGT1b was able to do so (Liu et al, pg 1490, right column, paragraph 2).

Plant SGT1 interacts with RAR1, SKP1 and HSP90 and all three of these proteins are involved in conferring disease resistance (Takahashi et al, 2003, Proc. Natl. Acad. Sci. USA 100:11777-11782, see pg 11781, left column, paragraph 2; Liu et al).

Thus, it is not clear that transformation of a plant with a nucleic acid encoding SEQ ID NO:8 will enhance disease resistance in a plant.

As the specification does not describe the transformation of any plant with SEQ ID NO:1 or nucleic acids that both interact with Rar1 and encode a maize protein that interacts with Rar1, that hybridize to SEQ ID NO:1 under “high stringency conditions”, that would be amplified from a maize nucleic acid library using primers that selectively hybridize under high stringency conditions to loci within SEQ ID NO:1, or that have 80% identity to SEQ ID NO:1, undue trial and error experimentation would be required to screen through the myriad of nucleic acids encompassed by the claims and plants transformed therewith, to identify those with modulated Rar-1 interactor protein or enhanced disease resistance, if such plants are even obtainable.

Given the claim breath, unpredictability in the art, undue experimentation, and lack of guidance in the specification as discussed above, the instant invention is not enabled throughout the full scope of the claims.

6. Claims 1-15 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter that was not described

in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are broadly drawn to a multitude of nucleic acids that interact with Rar1, that both interact with Rar1 and encode a maize protein that interacts with Rar1, that hybridize to SEQ ID NO:1 under “high stringency conditions”, that would be amplified from a maize nucleic acid library using primers that selectively hybridize under high stringency conditions to loci within SEQ ID NO:1, or that have 80% identity to SEQ ID NO:1. No such nucleic acid is described in the specification.

The specification does describe SEQ ID NO:1, but it does not interact with Rar1. The specification does not describe the structural features of any nucleic acids that can be amplified from a maize nucleic acid library using primers that selectively hybridize under high stringency conditions to loci within SEQ ID NO:1, nor are the primers or loci described.

If it is not the nucleic acid that interacts with Rar1, but the protein, claim 1, parts (a) and (c)-(e) do not recite the function of the protein encoded by the nucleic acid.

A wide range of proteins can interact with Rar1 at some point in the cell, including proteins involved in translation and degradation. The specification does not describe maize nucleic acids encoding such proteins within the full scope of the claims.

Hence, Applicant has not, in fact, described DNA molecules that interact with Rar1 or for nucleic acids that both interact with Rar1 and encode a maize protein that interacts with Rar1, and the specification fails to provide an adequate written description of the claimed invention.

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Therefore, given the lack of written description in the specification with regard to the structural and physical characteristics of the claimed compositions, it is not clear that Applicant was in possession of the genus claimed at the time this application was filed.

See *Univ. of California v. Eli Lilly*, 119 F.3d 1559, 43 USPQ 2d 1398 (Fed. Cir. 1997):

The name cDNA is not in itself a written description of that DNA; it conveys no distinguishing information concerning its identity. While the example provides a process for obtaining human insulin-encoding cDNA, there is no further information in the patent pertaining to that cDNA's relevant structural or physical characteristics; in other words, it thus does not describe human insulin cDNA Accordingly, the specification does not provide a written description of the invention

and at pg 1406:

a generic statement such as "vertebrate insulin cDNA" or "mammalian insulin cDNA," without more, is not an adequate written description of the genus because it does not distinguish the genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicted, does not suffice to define the genus because it is only an indication of what the genes does, not what it is.

... A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus.

... the claimed genera of vertebrate and mammal cDNA are not described by the general language of the '525 patent's written description supported only by the specific nucleotide sequence of rat insulin.

See *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ 2d 1016 at page 1021:

A gene is a chemical compound, albeit a complex one, and ... conception of a chemical compound requires that the inventor be able to define it so as to distinguish it from other materials Conception does not occur unless one has a mental picture of the structure of the chemical or is able to define it by its method of preparation, its physical or chemical properties, or whatever characteristics sufficiently distinguish it. It is not sufficient to define it solely by its principal biological property, *e.g.*, encoding human erythropoietin, because an alleged conception having no more specificity than that is simply a wish to know the identity of any material with that biological property.

7. The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

8. Claims 1-15 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that Applicant regards as the invention. Dependent claims are included in all rejections.

Claim 1 is indefinite in its recitation of both “an isolated nucleic acid capable of interacting with Rar1” in line 1 and “a polynucleotide encoding a maize Rar-1 interactor protein” in part (b). Is it the protein or the nucleic acid that interacts with Rar-1? Or does the nucleic acid both interact with Rar-1 AND encode a protein that also interacts with Rar-1 (part (b))? Furthermore, what is the nature of that interaction? Is an Rar-1 interactor a protein that only binds to Rar-1 or is it a protein that interacts with Rar-1 in any way (and thus including proteins like translation and degradation proteins. Similarly, in claims 9 and 13, it is not clear which, the protein, the nucleic acid or both, is the Rar-1 interactor.

Claim 1 is indefinite in its recitation of “selectively hybridize” in part (a). It is not clear what extent of hybridization is considered “selective”; thus, the metes and bounds of the claimed nucleic acid are unclear.

Claim 1 is indefinite in its recitation of “high stringency conditions” in parts (a) and (e). It is not clear what hybridization conditions are considered “high stringency”. The term is a relative term that is not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the metes and bounds of the invention.

Claim 3 lacks antecedent basis for the limitation “member of claim 1” as claim 1 is drawn to an isolated nucleic acid.

Claims 7, 10 and 14 are indefinite because a plant cannot be a maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and millet plant.

It is unclear if the seed of claim 8 comprises the recombinant expression cassette of claim 3 or if the seed is transgenic because it was transformed with another nucleic acid. Not all seeds from a transgenic plant will comprise the nucleic acid with which the plant was transformed.

Claims 9 and 13 lack antecedent basis for the limitation “Rar-1 interactor polynucleotide of claim 1” in part (a), as claim 1 is drawn to a nucleic acid.

In claims 9 and 13, parts (b), it is not clear if “plant growing conditions” would regenerate a plant from a plant cell, because the conditions required to grow a plant are different from the ones required to regenerate one. It is suggested that part (b) be replaced with --(b) regenerating a plant from the plant cell--.

In claims 9 and 13, parts (c), it is not clear what action the practitioner takes to induce expression of the polynucleotide. The promoter operably linked to it in part (a) is not an inducible promoter, which can be “induced” by the practitioner.

In claims 9 and 13, parts (c), it is not clear what it means to “modulate Rar1-interactor protein”. What is being done to it? What is being “modulated”? The protein activity? The level of the protein? Furthermore, claim 13 is drawn to a method of enhancing disease resistance in a plant, not to a method of modulating Rar-1-interactor protein.

Claim Rejections - 35 USC § 102

9. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

10. SEQ ID NO:2 corresponds to bases 1-571 of SEQ ID NO:7 and SEQ ID NO:3 corresponds to bases 1042-1430 of SEQ ID NO:7. SEQ ID NOs:2 and 3 are present in parent application 10/074,473, filed 12 February 2002; SEQ ID NOs:7-9 are not. Thus, the effective filing date for SEQ ID NOs:7-9 is the filing date of the instant application, 27 June 2003.

11. Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(a) as being anticipated by Hainey et al (October, 2002, GenBank Accession No. AY103953).

Hainey et al teach an isolated maize nucleic acid that has 98.7% identity to bases 24-1430 of SEQ ID NO:7 and 99.0% identity to bases 1-1086 of SEQ ID NO:9 (see sequence search results); this nucleic acid is part of a library and would thus be in a vector. It would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

12. Claims 1 and 16-17 are rejected under 35 U.S.C. 102(a) as being anticipated by Lai et al (2002, GenBank Accession No. CA401716).

Lai et al teach an isolated maize nucleic acid that has 99.3% identity to SEQ ID NO:7 (see sequence search results). It would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

13. Claims 1 and 16-17 are rejected under 35 U.S.C. 102(a) as being anticipated by Lai et al (3 June 2003 GenBank Accession No. CD443320).

Lai et al teach an isolated maize nucleic acid with 99.6% identity to bases 24-736 of SEQ ID NO:7 and 99.5% identity to bases 1-655 of SEQ ID NO:9 (see sequence search results). It

would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

14. Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(b) as being anticipated by Walbot et al (1999, GenBank Accession No. AW076372).

Walbot et al teach an isolated maize nucleic acid that has 99.8% identity to bases 735-1366 of SEQ ID NO:7 and 99.8% identity to bases 397-1050 of SEQ ID NO:9 (see sequence search results); this nucleic acid is part of a cDNA library and would thus be in a vector. It would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

15. Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(b) as being anticipated by Walbot et al (1999, GenBank Accession No. AW090936).

Walbot et al teach an isolated maize nucleic acid that has 99.8% identity to bases 121-965 of SEQ ID NO:7 and 99.8% identity to bases 240-884 of SEQ ID NO:9 (see sequence search results); this nucleic acid is part of a cDNA library and would thus be in a vector. It would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

16. Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(b) as being anticipated by Walbot et al (1999, GenBank Accession No. AW076374).

Walbot et al teach an isolated maize nucleic acid that has 99.7% identity to bases 478-1131 of SEQ ID NO:7 and 99.8% identity to SEQ ID NO:9 (see sequence search results); this nucleic acid is part of a cDNA library and would thus be in a vector. It would also hybridize to

SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

17. Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(b) as being anticipated by Walbot et al (1999, GenBank Accession No. AW155786).

Walbot et al teach an isolated maize nucleic acid that has 100.0% identity to bases 829-1455 of SEQ ID NO:7 (see sequence search results); this nucleic acid is part of a cDNA library and would thus be in a vector. It would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

18. Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(b) as being anticipated by Walbot et al (1999, GenBank Accession No. AW042392).

Walbot et al teach an isolated maize nucleic acid that has 99.8% identity to SEQ ID NO:7 and 99.7% identity to bases 147-732 of SEQ ID NO:9 (see sequence search results); this nucleic acid is part of a cDNA library and would thus be in a vector. It would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

19. Claims 1-6, 9, 11, 13 and 16-17 are rejected under 35 U.S.C. 102(a and e) as being anticipated by Liu et al, US2004/0034888A1, filed April 2003.

Liu et al teach isolated nucleic acids with 99.4%, 94.1%, 86.6% and 92.3% identity to SEQ ID NO:7 and 99.9%, 94.1%, and 99.4% identity to SEQ ID NO:9; the nucleic acids encode proteins with 100%, 93.5% and 93.1% identity to amino acids 1-361 of SEQ ID NO:8 (see sequence search results). They would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9.

Liu et al also teach recombinant DNA constructs comprising the nucleic acids and methods of using them to increase resistance to plant disease (claims 1-3).

20. Claims 1-6, 8-9, 11, 13 and 16-17 are rejected under 35 U.S.C. 102(a and e) as being anticipated by La Rosa et al, US2004/0214272, filed April 2003.

La Rosa et al teach isolated nucleic acids with 98.6% and 92.3% identity to SEQ ID NO:7 and 99.9%, 94.1% and 86.6% identity to SEQ ID NO:9 (see sequence search results). They would also hybridize to SEQ ID NOs:7 and 9 and could be amplified from a maize library using primers that hybridize to loci within SEQ ID NOs:7 or 9. La Rosa et al also teach recombinant DNA constructs comprising the nucleic acids and methods of using them to increase resistance to plant disease (claims 1-3).

21. Claims 1-6, 8-9, 11 and 13 are rejected under 35 U.S.C. 102(b) as being anticipated by Liu et al, July 2002, Plant Cell 14:1483-1496).

Liu et al teach isolated nucleic acids that would hybridize to SEQ ID NO:7 and 9 because they have regions of high identity (see sequence search results). Liu et al also teach tobacco plants transformed with the nucleic acids (pg 1490, right column, paragraphs 1-2).

22. Claims 12 and 15 are free of the prior art, given the failure of the prior art to teach or suggest a method of enhancing disease resistance or altering the level of anRar1-interactor protein by transformation with a nucleic acid of SEQ ID NO:2, 3 7 or 9. Claims 7, 10 and 14 are free of the prior art, given the failure of the prior art to teach or suggest plants that are maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and millet.

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Conclusion

23. No claim is allowed.

24. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Anne R. Kubelik, whose telephone number is (571) 272-0801. The examiner can normally be reached Monday through Friday, 8:30 am - 5:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson, can be reached at (571) 272-0804. The central fax number for official correspondence is (571) 273-8300.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.

Anne R. Kubelik, Ph.D.
May 6, 2005



ANNE KUBELIK, PH.D.
PRIMARY EXAMINER


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Db 125 LTFVPUKAEADGAARSVASFVEEKDAAAMONTPPMVE--VKPKYRHDFFYNSATEVLT 182
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Db 303 LEGDAALNKKFFRDYKDADDERAMMKSFVESNGTVLSTNNKWDGAKKVEGSPDGMEL 362
QY 357 KKWEY 361
Db 363 KKWEY 367

RESULT 4
Q84UV7
ID Q84UV7 PRELIMINARY; PRT; 370 AA.
AC Q84UV7;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE SGT1a.
OS Nicotiana benthamiana.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4100;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22115173; PubMed=12119369;
RA Liu Y., Schiff M., Serino G., Deng X.W., Dinesh-Kumar S.P.;
RT "Role of SCF ubiquitin-ligase and the COP9 signalosome in the N gene-
RL mediated resistance response to Tobacco mosaic virus.";
DR Plant Cell 14:1483-1496(2002).
DR EMBL; AF494083; AA085509.1; -.
DR InterPro; IPR007052; CS;
DR InterPro; IPR008978; HSP20_chap.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF04969; CS; 1.
DR Pfam; PF00515; TPR 1; 1.
DR SMART; SM00028; TPR 3.
DR PROSITE; PS50005; TPR; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Repeat; TPR repeat.
SQ SEQUENCE 370 AA; 41240 MW; 88EF4C3408F5121P CRC64;

Query Match 66.8%; Score 1243; DB 2; Length 370;
Best Local Similarity 66.2%; Pred. No. 7.5e-73;
Matches 245; Conservative 48; Mismatches 63; Indels 14; Gaps 5;

QY 3 ASDLESKAKAEFVDDDFELATYLSQADAGPATADLYADRAQAHIKLGNYTEAVDANK 62
Db 2 ASDLETRAKAEFIDHDELAVDLITQALAMTPKNKAELEFADRAQAHIKLGNYTEAVDANK 61
QY 63 AIELDPMHKAAYRKGAACIKLEEYOTAKAALGSSYASGDSRPARLLKCEDERIAEES 122
Db 62 AIELDPSMSKAYLRKGLAKMKLEEYOTAKAALGASLPAESRFTKLIKCEDERIAEEA 121
QY 123 SQAPVKNVEATVAATIED--KEPTNMENTPPVIEP-----PSKPKYRHDYNSAT 171
Db 122 GELNPSVDKTSNGVNPAPPASESLDNVAVAPKDAQPTVNLISQCSAARPKYRHEFYQKPE 181
QY 172 EVLVTTFAGKVPADSVVWIDFGEQMLSVSIEVPGEPYHFQPLRFSKIIPKCKYQVLTSTK 231
Db 182 EVVVTTFAGKIPAKNVVVDVDFGEQMLSVSIVDPGDTYSFQPLRFGKITPAKCRFYMSTK 241
QY 232 VEIRLAKAEQVTTWTLDSGRPKTVPOKISTPAETAPRPSYPSSKAKK--DWDKLEAEVKK 290

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Db 242 IEIRLAKAEPLHTWTSLEIT--RASVVQRPNVSSD--APRPSYSSKURHVDWDKLEAEVKK 299
QY 291 EKKEEKLGDGAALNKKFFRDYKDADDERAMMKSFVESNGTVLSTNNKWDGAKKVEGSP 350
Db 300 ESKDEKLGDGAALNKKFFRDYKDADDERAMMKSFVESNGTVLSTNNKVEGTVKKEGSP 359
QY 351 PDGMELKKWE 360
Db 360 PDGMELKKWE 369

RESULT 5
Q8WS15
ID Q8WS15 PRELIMINARY; PRT; 350 AA.
AC Q8WS15;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE SGT1a.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21893744; PubMed=11847307; DOI=10.1126/science.1067554;
RA Azevedo C., Sadanandom A., Kitagawa K., Freialdenhoven A., Shirasu K.,
RA Schulze-Lefert P.;
RT "The RAR1 interactor SGT1, an essential component of R gene-triggered
RT disease resistance.";
RL Science 295:2073-2076(2002).
DR EMBL; AF439975; AAL33611.1; -.
DR HSP; P31948; 1ELW.
DR Pfam; PF04969; CS; 1.
DR Pfam; PF05002; SGS; 1.
DR Pfam; PF00515; TPR 1; 2.
DR SMART; SM00028; TPR; 3.
DR PROSITE; PS50005; TPR; 2.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Repeat; TPR repeat.
SQ SEQUENCE 350 AA; 39277 MW; D23DBE990C817FB4 CRC64;

Query Match 61.4%; Score 1142; DB 2; Length 350;
Best Local Similarity 61.7%; Pred. No. 2.6e-66;
Matches 222; Conservative 56; Mismatches 68; Indels 14; Gaps 4;

QY 3 ASDLESKAKAEFVDDDFELATYLSQADAGPATADLYADRAQAHIKLGNYTEAVDANK 62
Db 2 AKELADKAKAEFVDDDFDVAVDLYSKAIDLDPNCABFFADRAQAHIKLESFTEAVDANK 61
QY 63 AIELDPMHKAAYRKGAACIKLEEYOTAKAALGSSYASGDSRPARLLKCEDERIAEES 122
Db 62 AIELDPSLTAKAYLRKGTACMKLEEYRTAKTALSKASITPESKFKKLIDECNFLTTEE 121
QY 123 SQAPVKNVEATVAATIEDKEDFTNMENTPPVIEPPSKP--KYRHDYNSATEVLTIFAK 180
Db 122 KDL-VQPVSTLPSV-----TAPVSELDVTPAKYRHEFYQKPEVVVTVFAK 170
QY 181 GVPADSVVWIDFGEQMLSVSIEVPGEPYHFQPLRFSKIIPKCKYQVLTSTKVEIRLAKAE 240
Db 171 GIPKQNVNIDFGEQILSVVIEVPGEDAYVLPRLFGKIIPDKCKYEVLTSTKIEIRLAKAD 230
QY 241 QVTTWTLDSGRPKTVPOKISTPAETAPRPSYPSSKAKDWDKLEAEVKKKEEKLDGD 300
Db 231 IITWASLEHGKGPVLP--KPNVSSEVSQRPAYSSKKVWDKLEAEVKKQEKDEKLEG 289
QY 301 AALNKKFFRDYKDADDERAMMKSFVESNGTVLSTNNKWDGAKKVEGSPDGMELKKWE 360
Db 290 AALNKKFFRIYQNAEDDERAMKSFVESNGTVLSTNNKVEGTVKTIESTPPDGMELKKWE 349

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At 56T1A

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 20, 2005, 18:18:25 ; Search time 40 Seconds
(without alignments)
868.356 Million cell updates/sec

Title: US-10-609-078-8
Perfect score: 1861
Sequence: 1 MAASLESKAKEAFVDDDFE.....GAKKVEGPPDGMELKKWEY 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1135	61.0	358	2 T13017	hypothetical prote
2	1134	60.9	350	2 T05589	hypothetical prote
3	383	20.6	198	2 T20305	hypothetical prote
4	364.5	19.6	395	2 S66940	SGT1 protein - yea
5	341	18.3	444	2 T40307	hypothetical prote
6	327	17.6	469	2 T48783	related to SGT1 pr
7	223	12.0	533	2 E84858	phosphoprotein pho
8	193.5	10.4	572	2 H86257	protein F5011.2 [i
9	192	10.3	498	1 S52570	phosphoprotein pho
10	187	10.0	358	2 T00954	hypothetical prote
11	186	10.0	499	1 A55346	phosphoprotein pho
12	181.5	9.8	543	2 A38093	transformation-sen
13	180.5	9.7	473	1 T40391	phosphoprotein pho
14	177.5	9.5	589	2 A32567	stress-induced pro
15	176	9.5	569	2 S56658	stress-induced pro
16	174	9.3	349	2 T08782	hypothetical prote
17	174	9.3	526	1 T45058	phosphoprotein pho
18	169.5	9.1	513	1 S52571	phosphoprotein pho
19	163.5	8.8	346	2 S61991	hypothetical prote
20	163.5	8.8	591	2 T41531	activator of Hsp70
21	161.5	8.7	558	2 T48150	stress-induced pro
22	160	8.6	627	2 T04562	hypothetical prote
23	159.5	8.6	479	1 T46576	phosphoprotein pho
24	159.5	8.6	591	2 T51996	hypothetical prote
25	157.5	8.5	901	2 JC7111	tetratricopeptide
26	151	8.1	677	2 T45682	hypothetical prote
27	148.5	8.0	358	2 T37805	hypothetical prote
28	147	7.9	317	2 T37851	hypothetical prote
29	146.5	7.9	385	2 S40899	hypothetical prote

30	145.5	7.8	422	2 T24865	hypothetical prote
31	141.5	7.6	1979	2 JMW059	mtprd protein - mo
32	139	7.5	605	2 AF1917	hypothetical prote
33	139	7.5	781	2 F86457	unknown protein, 3
34	137.5	7.4	547	2 AE1884	hypothetical prote
35	136.5	7.3	222	2 F86424	unknown protein, 6
36	136	7.3	225	2 AB2539	hypothetical prote
37	132.5	7.1	320	2 T03899	hypothetical prote
38	130.5	7.0	297	2 T34141	hypothetical prote
39	130.5	7.0	1621	2 AB2255	72K mitochondrial
40	130	7.0	619	2 A36682	tetratricopeptide
41	130	7.0	2025	2 JC5020	extracellular matr
42	130	7.0	2055	2 T31110	hypothetical prote
43	129.5	7.0	427	2 T00960	class I heat-shock
44	129.5	7.0	542	2 AD1333	unc-45 protein - C
45	127.5	6.9	961	2 T32493	

ALIGNMENTS

RESULT 1

T13017

hypothetical protein F8L21.50 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: T13017

R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirks, W.; Stiekema, W.; Bancroft, I.; Mc

A:Reference number: Z17587

A:Accession: T13017

A:Molecule type: DNA

A:Residues: 1-358 <BEV>

A:Cross-references: UNIPROT:Q9SUT5; EMBL:AL096882; GSPDB:GNO0062; ATSP:F8L21.50

A:Experimental source: cultivar Columbia; BAC clone F8L21

C:Genetics:

A:Gene: ATSP:F8L21.50

A:Map position: 4

A:Introns: 54/1, 77/2; 119/1, 161/2; 193/3; 215/3; 262/1; 288/3; 323/3

Query Match 61.0%; Score 1135; DB 2; Length 358;

Best Local Similarity 61.0%; Pred. No. 1.5e-69;

Matches 224; Conservative 49; Mismatches 76; Indels 18; Gaps 4;

QY	3	ASDLESKAKEAFVDDDFELATLYSQADAGATADLVADRAQAHIKLGNYTEAVDANK	62
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QY	63	ATELDPMHKAAYRGAACIKLEBYQTAKAALGLSSVAGSGRSFARLLKCEDERIAES	122
DB	62	AIELEPTLAKVLRGTACMKLEESTAKALEKASVAPNEPKFKMIDCDLRAESE	121
QY	123	SQ-----APVKNVBEATVAATIEDKEDFTNMENPPVIEP--PSKPKYRHDYNSATEVV	174
DB	122	KDLVQPMPPSLPSSSTTTPLATEAD-----APPVPIPAAPAKPMFHFYQKPEEAV	172
QY	175	LTFPAKVPADSVVDVDFEQMLSVIEVPGEPYHFORLPSKIIPECKYVLSKVEI	234
DB	173	VTIFAKVPKENVTYVFEQSILVVDVAGEAYHLQRLFKIIPKCRFVLSKVEI	232
QY	235	RLAKAEQVTTTLDYSGRPKTPVQKISTPAETAPRPSYSSKAKDWDKLEAEVKKEE	294
DB	233	RLAKAEITWASLEY-GKQSVLPKPNVSSALSQRPVFPSSPKAKDWDKLEAEVKKEKD	291
QY	295	EKLDGDAALNKPFRDIYKDADEDMRRAMKSVESNGTVLSTNWKDVGAKKVEGSPDGM	354
DB	292	EKLDGDAAMKFFSDIYSSADEDMRRAMKSVESNGTVLSTNWKVEGTVKKEVSTPDGM	351
QY	355	ELKKWEY 361	
DB	352	ELKKWEY 358	

D**b** 254 GGCCGCGTCCGATCTGGAGAGCAAGGCCAAGGAGGCCCTTCGTGACGACGACTTCGAGCT 31

Qy	444	ATCTAGCCAGGCA	CCAGTAAAGAA	TTTGAGGCTA	CTGTGGCTGCTA	CTATTGAGGACAA	503					
Db	445	ATCTAGCCAGGCA	CCAGTAAAGAA	TTTGAGGCTA	CTGTGGCTGCTA	CTATTGAGGACAA	504					
Qy	504	GGAGGATTTCA	CAAAATATCGGA	ATACACCA	CCAGTGATAGAAC	CCCCCAAGCAACCAAA	563					
Db	505	GGAGGATTTCA	CAAAATATCGGA	ATACACCA	CCAGTGATAGAAC	CCCCCAAGCAACCAAA	564					
Qy	564	ATACAGGCATG	ACTACTACA	CAACAGTGCC	ACAGAAAGTGTA	CTGCACAATATTTGCTAAAGG	623					
Db	565	ATACAGGCATG	ACTACTACA	CAACAGTGCC	ACAGAAAGTGTA	CTGCACAATATTTGCTAAAGG	624					
Qy	624	TGTTCTCTGCT	GTAGTGTAGT	CAATTGA	TTTTGGTGAAC	AGATGTTGAGTGTA	TCATTGA	683				
Db	625	TGTTCTCTGCT	GTAGTGTAGT	CAATTGA	TTTTGGTGAAC	AGATGTTGAGTGTA	TCATTGA	684				
Qy	684	AGTTCTCTG	TGAAGAA	CCATAC	ATTTTCAG	CCCCCGTCTGT	TTTCTAGATAT	CCCTGA	743			
Db	685	AGTTCTCTG	TGAAGAA	CCATAC	ATTTTCAG	CCCCCGTCTGT	TTTCTAGATAT	CCCTGA	744			
Qy	744	GAATGCAAA	TATCAAGT	CTTATCCA	CAAGGTTGAA	ATA	CGCCTTGCAAA	AGCTGAGCA	803			
Db	745	GAATGCAAA	TATCAAGT	CTTATCCA	CAAGGTTGAA	ATA	CGCCTTGCAAA	AGCTGAGCA	804			
Qy	804	GGTGACATG	GCAACCC	TGGATAT	AGTGGGAAG	CAAAAGACTGT	TCCCCCAAGAGAT	TAAG	863			
Db	805	GGTGACATG	GCAACCC	TGGATAT	AGTGGGAAG	CAAAAGACTGT	TCCCCCAAGAGAT	TAAG	864			
Qy	864	CAGCCAGT	GAAACAG	CCCCCAAG	CACTTCAT	ACCCATCTTCAA	AGGGGCAAAAAG	ACTG	923			
Db	865	CAGCCAGT	GAAACAG	CCCCCAAG	CACTTCAT	ACCCATCTTCAA	AGGGGCAAAAAG	ACTG	924			
Qy	924	GGATAACT	TGAA	GCTGAAGT	CAAAAGG	AGGAGGAAG	GAAGAA	AAACTTGTAT	GTGTGATGC	983		
Db	925	GGATAACT	TGAA	GCTGAAGT	CAAAAGG	AGGAGGAAG	GAAGAA	AAACTTGTAT	GTGTGATGC	984		
Qy	984	TGCATTGAA	CAAA	TTCTTCC	GTGACATCTA	CAAGGATGCT	CA	TGAGATAT	CGCGAGGC	1043		
Db	985	TGCATTGAA	CAAA	TTCTTCC	GTGACATCTA	CAAGGATGCT	CA	TGAGATAT	CGCGAGGC	1044		
Qy	1044	CATGATGA	AGTCA	TTCTG	TGGAA	TCAAA	TGGCA	CTGTTCTCTCA	ACCAAT	TGGAAGATGT	1103	
Db	1045	CATGATGA	AGTCA	TTCTG	TGGAA	TCAAA	TGGCA	CTGTTCTCTCA	ACCAAT	TGGAAGATGT	1104	
Qy	1104	TGGAGCA	AGAGGT	AGAGG	AGCCCCCT	GTATGGTA	TGAGCTCA	AGAGTGGGA	TA	1163		
Db	1105	TGGAGCA	AGAGGT	AGAGG	AGCCCCCT	GTATGGTA	TGAGCTCA	AGAGTGGGA	TA	1164		
Qy	1164	CTAAAGTTT	TGGA	CTGCCG	CTTTTGT	TAAATCC	CAGGTC	TTTGGAA	ACTATG	CACTTAATCT	1223	
Db	1165	CTAAAGTTT	TGGA	CTGCCG	CTTTTGT	TAAATCC	CAGGTC	TTTGGAA	ACTATG	CACTTAATCT	1224	
Qy	1224	GCCCA	CCCATAG	TGCCAT	AGCTTG	CTTGTTA	AGTCTCTG	CTTTTGTAA	AGCTTTCT	GTGA	1283	
Db	1225	GTCAC	CCCATAG	TGCCAT	AGCTTG	CTTGTTA	AGTCTCTG	CTTTTGTAA	AGCTTTCT	GTGA	1284	
Qy	1284	TGACAGT	CTAG	CGTGTCT	GTAGTG	CTACT	TTGCGGTAG	CTTTTGA	TGGA	CATAGGTATGC	1343	
Db	1285	TGACAGT	CTAG	CGTGTCT	GTAGTG	CTACT	TTGCGGTAG	CTTTTGA	TGGA	CATAGGTATGC	1344	
Qy	1344	TATTAT	TGTGTAT	CGAC	CCCCGAA	CACTCT	GTGTAT	CAAA	AGACAG	CAAACTATAA	TGTAT	1403
Db	1345	TATTAT	TGTGTAT	CGAC	CCCCGAA	CACTCT	GTGTAT	CAAA	AGACAG	CAAACTATAA	TGTAT	1404
Qy	1404	GGAA	TGCTAT	CTTTT	TGTTG	CTAA	AA	1430				
Db	1405	GGAA	TGCTAT	CTTTT	TGTTG	CTAA	AA	1431				

RESULT 3

US-10-425-114-25244

; Sequence 25244, Application US/10425114

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; Publication No. US20040034888A1
;
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabasta, Jack E
; APPLICANT: Cao, Yongwei
;
; TITLE OF INVENTION: Nucleic Acid
;
; FILE OF INVENTION: Plants and
; CURRENT APPLICATION: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US
; CURRENT FILING DATE: 2003-04-
; NUMBER OF SEQ ID NOS: 73128
;
; SEQ ID NO 25244
;
; LENGTH: 1450
;
; TYPE: DNA
;
; ORGANISM: Zea mays
;
; FEATURE:
;
; OTHER INFORMATION: Clone ID: I
US-10-4295-114-25244

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Query Match	95.8%	Score 1394.2	DB 17	Length 1450	
Best Local Similarity	99.4%	Pred. No. 0			
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QY	24	AGTCATCGTCTGTCGTCGCCGCGAGAGGGCGACAGCCCAAGCCCGAAGGGCGCCAT	83		
Db	31				
QY	84	GGCCGCGTCTGGATCTGGAGAGCAAGGCCAAGAGGGCCCTTCGTCCACACACGACTTCGAGCT	143		
Db	91				
QY	144	GGCCAACGAGCTCTACAGCAGGCCATCGACCGCGGGCCGCCACCGCCGACCTCTATGC	203		
Db	151				
QY	204	CGACCGCGCCGCGCGCACATCAAGCTCGGCCAACTACACTGAGGCTGTGGCGGATGCTAA	263		
Db	211				
QY	264	CAAAAGCAATTGAGCTTGATCCTATGATGCATAAAGCTTACTACCGGAAAGGTGCTGCATG	323		
Db	271				
QY	324	CATTTAAGCTTGAGATACCAACTGCAAGGCTGCTCTTGAGTTGGGTTCTTCTTATGC	383		
Db	331				

Qy	384	ATCAGGCGATTCAAGGTTTGCTCGTCTATTGAAGGAATGTGATGAGCGCATCGCTGAGGA	443
Db	391	ATCAGGCGATTCAAGGTTTGCTCGTCTATTGAAGGAATGTGATGAGCGCATCGCTGAGGA	450
Qy	444	ATCTAGCCAGGCAACCGATTAAGAATGTGAGGCTACTGTGGTGCTACTATTGAGGACAA	503
Db	451	ATCTAGCCAGGCAACCGATTAAGAATGTGAGGCTACTGTGGTGCTACTATTGAGGACAA	510
Qy	504	GGAGGATTTTCACAAATATGGAGAAATACACCAACAGTGATAGAACCCCAAGCAAAACCAA	563
Db	511	GGAGGATTTTCACAAATATGGAGAAATACACCAACAGTGATAGAACCCCAAGCAAAACCAA	570
Qy	564	ATACAGGCATGACTACTACAAACAGTGCCCAAGAGTGGTACTGACAAATATTTGCTTAAGG	623
Db	571	ATACAGGCATGACTACTACAAACAGTGCCCAAGAGTGGTACTGACAAATATTTGCTTAAGG	630
Qy	624	TGTTCTGCTGATAGTGATGTCATTGATTTTGGTGAAACAGATGTTGAGTGATCCATTGA	683
Db	631	TGTTCTGCTGATAGTGATGTCATTGATTTTGGTGAAACAGATGTTGAGTGATCCATTGA	690
Qy	684	AGTTCTGCTGAGAAACCAATACATTTTCAGCCCCGTCTGTTTTCTAAGATTTATCCCTGA	743
Db	691	AGTTCTGCTGAGAAACCAATACATTTTCAGCCCCGTCTGTTTTCTAAGATTTATCCCTGA	750


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Db 1053 GTGGAAGACCAAGACTGTTCCCAAGAGATAAGCAGCGCAGCTGAAACAGGCCCAAGAC 1112
Qy 890 CTTTATACCCATCTTCAAGGCGAAAGAAAGACTGGGATAAACTGGAAGCTGAAGTCAAAA 949
Db 1113 CTTTATACCCATCTTCAAGGCGAAAGAAAGACTGGGATAAACTGGAAGCTGAAGTCAAAA 1172
Qy 950 AGGAGAGAGAGAGAAAGAACTTGATGGTGTGATGCTGCAATGAACAAATCTTCCGTGACA 1009
Db 1173 AGGAGAGAGAGAGAAAGAACTTGATGGTGTGATGCTGCAATGAACAAATCTTCCGTGACA 1232
Qy 1010 TCTACAAGATGCTGATGAAGATATGCGGAGGGCCCATGATGAAGTCAATTCGTGGATCAA 1069
Db 1233 TCTACAAGATGCTGATGAAGATATGCGGAGGGCCCATGATGAAGTCAATTCGTGGATCAA 1292
Qy 1070 ATGGCACTGTTCTCTCAACCAATTCGAAGATGTTGGAGCAAGAGGTAGAGGGAGCC 1129
Db 1293 ATGGCACTGTTCTCTCAACCAATTCGAAGATGTTGGAGCAAGAGGTAGAGGGAGCC 1352
Qy 1130 CCCCTGATGTTAGTGAAGTCAAGAAAGTGGGAATATAAAAGTTTGACCTGCCGTCTTTTG 1189
Db 1353 CCCCTGATGTTAGTGAAGTCAAGAAAGTGGGAATATAAAAGTTTGACCTGCCGTCTTTTG 1412
Qy 1190 TAAATCCAGGCTTGGAAACTATGACCTAATTCGCCCAACCATAGTGCCTGAGCTTGC 1249
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Qy 1250 TTGGTTAAGTCTCTCTTTGTAAGCTTCTGTATGACAGTCTAGCGGTGTCTGAGTGC 1309
Db 1473 TTGGTTAAGTCTCTCTTTGTAAGCTTCTGTATGACAGTCTAGCGGTGTCTGAGTGC 1532
Qy 1310 TACTTGCCTGATGTTTGTATGACATAGTATGCTATTAATGTTGGTATCGACCCCGAACCA 1369
Db 1533 TACTTGCCTGATGTTTGTATGACATAGTATGCTATTAATGTTGGTATCGACCCCGAACCA 1592
Qy 1370 TCTGTGGTATCAAGACAGCAACTATTAATGATGGAATGCTATCTTTTGTGCTTAAA 1429
Db 1593 TCTGTGGTATCAAGACAGCAACTATTAATGATGGAATGCTATCTTTTGTGCTTAAA 1652
Qy 1430 AAAAAAAAAAAAAAAAAAAAAA 1455
Db 1653 AAAAAAAAAAAAAAAAAAAGCGCGCAAAA 1678
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RESULT 5

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US-10-425-114-24871
; Sequence 24871, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 24871
; LENGTH: 1649
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-210-C7_FLI
US-10-425-114-24871
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Query Match 81.0%; Score 1179; DB 17; Length 1649;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 1403; Conservative 0; Mismatches 0; Indels 214; Gaps 1;
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Qy 24 AGTCATCGTCTGGTCTGTCGCCGAGAGCGCAGACGCCCAAGAGCGGCGCCCAT 83
Db 33 AGTCATCGTCTGGTCTGTCGCCGAGAGCGCAGACGCCCAAGAGCGGCGCCCAT 92
Qy 84 GSCCGCTCGATCTGGAGAGCAAGGCCCAAGAGGCCCTTCTGTCAGAGCAGCTTCGAGCT 143
Db 93 GSCCGCTCGATCTGGAGAGCAAGGCCCAAGAGGCCCTTCTGTCAGAGCAGCTTCGAGCT 152
Qy 144 GSCCACCCGAGCTCTACAGCCAGGCGCATCGAGCGCGGGCCCGCCACCGCGGACCTCTATGC 203
Db 153 GSCCACCCGAGCTCTACAGCCAGGCGCATCGAGCGCGGGCCCGCCACCGCGGACCTCTATGC 212
Qy 204 CGACCGGCGCCCAAGCGGCGCATCAAGCTCGGCAACTACACTGAGGCTGTGGCGGATGCTTAA 263
Db 213 CGACCGGCGCCCAAGCGGCGCATCAAGCTCGGCAACTACACTGAGGCTGTGGCGGATGCTTAA 272
Qy 264 CAAAGCAATTGAGCTTGTATCTATGATGATCAAAAGCTTACTACCGGAAGGTGCTGATG 323
Db 273 CAAAGCAATTGAGCTTGTATCTATGATGATCAAAAGCTTACTACCGGAAGGTGCTGATG 332
Qy 324 CATTAAAGCTTGAAGAAATACCAAACTGCAAAAGCTGCTCTTTCAGTTGGGTTCTTCTTATGC 383
Db 333 CATTAAAGCTTGAAGAAATACCAAACTGCAAAAGCTGCTCTTTCAGTTGGGTTCTTCTTATGC 392
Qy 384 ATCAGGCGAATCAAGGTTTGTCTCTATTGAAGAAATGTGATGAGCGCATCGCT- 438
Db 393 ATCAGGCGAATCAAGGTTTGTCTCTATTGAAGAAATGTGATGAGCGCATCGCTGGTGA 452
Qy 439 - 438
Db 453 GAAAAATTAACTTCAGCAGTGTGTGTATCTGCTGGTGGTGTGGGTCTTGGGTATGC 512
Qy 439 - 438
Db 513 AATGTGTGATGCTATTTTCTGACGATATGATGCTCAGCTAGCTGCTTCTCTGAGAAAT 572
Qy 439 - 438
Db 573 GTTTGTAGCAGCTTGTAGACTGGGGATGATTATGTTTCAGCTTAACTATCATCTCATCTA 632
Qy 439 - GAGGAATCTAGCCAGGCAACCGAGTAAGAAATG 469
Db 633 CTTGTCTATGTTATTTTGTATGTTTCCAGAGGAATCTAGCCAGGCAACCGAGTAAGAAATG 692
Qy 470 TTGAGGCTTACTGTGGTGTCTTACTATTGAGGACAGGAGGAGGATTTTCCAAAATATGAGAAATA 529
Db 693 TTGAGGCTTACTGTGGTGTCTTACTATTGAGGACAGGAGGAGGATTTTCCAAAATATGAGAAATA 752
Qy 530 CACCACCAAGTATAGAAACCCCGCAAGCAAAACCAAAATACAGGCATGACTACTACACAGTG 589
Db 753 CACCACCAAGTATAGAAACCCCGCAAGCAAAACCAAAATACAGGCATGACTACTACACAGTG 812
Qy 590 CCACAGAGTGGTACTGACAAATATTTGCTAAGGGTGTCTCTGATAGTGTAGTCTATTG 649
Db 813 CCACAGAGTGGTACTGACAAATATTTGCTAAGGGTGTCTCTGATAGTGTAGTCTATTG 872
Qy 650 ATTTTGGTGAACAGATGTCAGTGTATCCATTCAGTTTCTGTTGGTGAAGAACCATACCATTT 709
Db 873 ATTTTGGTGAACAGATGTCAGTGTATCCATTCAGTTTCTGTTGGTGAAGAACCATACCATTT 932
Qy 710 TTCAGCCCCCTCTGTTTCTTAAGATATCCCTGAGAAATGCAAAATATCAAGTCTTATCCA 769
Db 933 TTCAGCCCCCTCTGTTTCTTAAGATATCCCTGAGAAATGCAAAATATCAAGTCTTATCCA 992
Qy 770 CCAAGGTTGAATATACGCTTTCGAAAAGCTGAGCAGGTGACATGGACAAACCTCGGATTTA 829
Db 993 CCAAGGTTGAATATACGCTTTCGAAAAGCTGAGCAGGTGACATGGACAAACCTCGGATTTA 1052
Qy 830 GTGGAAGACCAAGAGCTGTTCCCGCAGAGTATAGCAGCGCGAGCTGAAAACAGCCCCAGAC 889
Db 1053 GTGGAAGACCAAGAGCTGTTTCCCGCAGAGTATAGCAGCGCGAGCTGAAAACAGCCCCAGAC 1112
Qy 890 CTTTCATACCATCTTCAAAAGGCGAAAAAAGACTGGGATAAACTGGAAGCTGAAGTCAAAA 949
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231 CGGCAACTTACACTGAGGCTGTGGCGGATGCTAAACAGCAATTGAGCTTGTATCTTATGAT 290

243 CGGCAACTTACACTGAGGCTGTGGCGGATGCTAAACAGCAATTGAGCTTGTATCTTATGAT 302

291 GATTAAGCTTACTACCGGAAGGTGCTGCATGCATTAAGCTTTGAAGAATACCAAACTGC 350

303 GCATTAAGCTTACTACCGGAAGGTGCTGCATGCATTAAGCTTTGAAGAATACCAAACTGC 362

351 AAAGGCTGCTCTTGAAGTTGGGTTCTTCTTATGCATCAGGCGAATCAAGGTTTCTCGTCT 410

363 AAAGGCTGCTCTTGAAGTTGGGTTCTTCTTATGCATCAGGCGAATCAAGGTTTCTCGTCT 422

411 ATTGAAGGAATGTGATGAGCGCATCGCTAGCAATCTAGCCAGGCAACGATGAAGAATGT 470

423 ATTGAAGGAATGTGAAGAGCGCATTTGCTAGGGAATCTAGCCAGGCTCCAGCAAGAATGT 482

471 TGAGGCTTACTGTG-----GCTGCTACTATTGAGCAAGGAGGATTTCAAAATAT 521

483 TGAGGCTTCTTGTGGCTGCTGCTACTTGTAGGCAAGGAGGATGTGCAATAT 542

521 GGAGGAATACACACAGTGTAGAACCCCAAGCAAAACCAAAATAACGAGCATGACTACTA 581

602 GGAGGAATACACCCGACAGTGTAGAACCCCAAGCAAAACCTAATATGTCCTGACTACTA 641

543 GGAGGAATACACCCGACAGTGTAGAACCCCAAGCAAAACCTAATATGTCCTGACTAGTGT 641

582 CAAACGTGCCACAGAGTGTGATGACAAATTTGCTAAGGCTGTTCTGCTGATAGTGT 662

603 CAAACAGTGCCACAGAGTGTGTTTGACAAATTTGCTAAGGCTGTTCCGCTGATAGTGT 662

642 AGTCATTCATTTTGGTGAACAGATGTTGAGTGTATCCATTTGAAGTTCCTGCTGGAAGACC 701

663 AGTCATTTGTTGGTGAACAGATGTTAAGTGTGTCATTTGAAGTTCCTGCTGGAAGACC 722

702 ATACCAATTTGACGCCGCTGTTTCTTAAGATATTCCTTGAGAAATCAAAATATCAAGT 761

723 ATACCAATTTGACGCCGCTGTTTGTGTAGATATCCCTTGAGAAATGCAAAATATCAAGT 782

762 CTTATCCCAAGGTTGAAATACGCTTTGCAAAAGCTGACAGGTGACATGGCAACACCT 821

783 CTTGTCCACAGGTCGAATACGCTTTGCAAAAGCTGACAGGTGACATGGCAACACCT 842

822 GGATATATGTTGAAGACCAAGACGTTTCCCAAGAGATGAACGACGCGAGCTGAACACG 891

843 GGATATATGTTGAAGACCAAGGCTTTCCCAAGAGATGAACGACGCGAGCTGAACACG 902

882 CCCAAGACCTTCATCCCATCTTCAAGGCGCAAAAGACCTGGGATTAACCTGGAGCTGA 941

903 CCCAAGACCTTCATCCCATCTTCAAGGCGCAAAAGACCTGGGATTAACCTGGAGCTGA 962

942 AGTCAAAAAGGAGAGAGAGAGAAAACTTGATGCTGATCTGCATTTGAACAAATCTT 1001

963 AGTCAAAAAGGAGAGAGAGAGAAAACTTGATGCTGATCTGCATTTGAACAAATCTT 1022

1002 CCGTGACATCTACAAGATCTGATGAAGATATGCGAGGCGCATGTAAGTCAATTCGT 1061

1023 CCGTGACATCTACAAGATCTGATGAAGATATGCGAGGCGCATGTAAGTCAATTCGT 1082

1062 GGAATCAAAATGGCACTGTTCTTCAACCAATTTGGAAGATGTTGGAGCAAAAGAGTGA 1121

1083 GGAATCTAAATGGCACTGTTCTTCAACCAATTTGGAAGATGTTGGAGCAAAAGAGTGA 1142

1122 AGGAGGCCCCCTGATGATGATGAGCTCAAGAGTGGATATCTAAAGTTTGGAC-TGCC 1180

1143 AGGAGGCCCTCTGATGATGATGAGCTCAAGAGTGGATATCTAAAGTTTGGAC-TGCC 1202

1181 CGTCTTTTGTAAATCCAGTCTTTGGAAGATTTAGATCTAGTAACGTCACCCATTTGGGT 1262

1203 CGTCTTTTGTAAATCCAGTCTTTGGAAGATTTAGATCTAGTAACGTCACCCATTTGGGT 1262

1240 ATGAGCTTGCCTGGTTTAAAGTCTCTGCTTTTGTGTAAGCTTTCTGATGACGCTAGCGTGT 1299

1263 GCTGAGCTTGGTTTAAAGTCTCTGCTTTTGTGTAAGCTTTCTGATGACGCTAGCGTGT 1320

db	1113	CTTCATACCCATCTTCAAAAGGCGAAAAAGACTGGGATAAACTGGAACTGGAAGCTGAAGTCAAAA	1172
2y	950	AGGAGGAGAGGAGAGAAAACCTTGATGGTGATGCTGCATTGAAACAAATCTTCCGTGACA	1009
db	1173	AGGAGGAGAGGAGAGAAACCTTGATGGTGATGCTGCATTGAAACAAATCTTCCGTGACA	1232
Qy	1010	TCTACAAGGATGCTGATGAAGATATGCGGAGGGCCATGATGNAAGTCAATCGTGGAAATCAA	1069
db	1233	TCTACAAGGATGCTGATGAAGATATGCGGAGGGCCATGATGNAAGTCAATCGTGGAAATCAA	1292
Qy	1070	ATGGCACTGTTCTCTCAACCAATGGAAAGATGTTGGAGCGAAAGAGGTAGAAGGGAGCC	1129
db	1293	ATGGCACTGTTCTCTCAACCAATGGAAAGATGTTGGAGCGAAAGAGGTAGAAGGGAGCC	1352
Qy	1130	CCCCTGATGGTATGGAGCTCAAGAGTGGGAATACTAAAGTTTGACCTGCCCGTCTTTTG	1189
db	1353	CCCCTGATGGTATGGAGCTCAAGAGTGGGAATACTAAAGTTTGACCTGCCCGTCTTTTG	1412
Qy	1190	TAAATCCAGGTCCTGGAACTATGACCTAAATCTGCCCAACCATAGTGCATGAGCTTGC	1249
db	1413	TAAATCCAGGTCCTGGAACTATGACCTAAATCTGCCCAACCATAGTGCATGAGCTTGC	1472
Qy	1250	TGGTTAAGTCTCTGCTTTTGTGAAGCTTTCGTATGACAGTCTAGCGGTGTCGTAGTGC	1309
db	1473	TGGTTAAGTCTCTGCTTTTGTGAAGCTTTCGTATGACAGTCTAGCGGTGTCGTAGTGC	1532
Qy	1310	TACTTGCCTAGCTTTTGATGGACATAGGTATGCTATTATGTGGTATCGACCCCGAACCA	1369
db	1533	TACTTGCCTAGCTTTTGATGGACATAGGTATGCTATTATGTGGTATCGACCCCGAACCA	1592
Qy	1370	TCTGTGGTATCAAAGACAGCAAACTATAATGTATGGAAATGCCCTATTCCTTTTGGTCT	1426
db	1593	TCTGTGGTATCAAAGACAGCAAACTATAATGTATGGAAATGCCCTATTCCTTTTGGTCT	1649

RESULT 6
 US-10-767-701-13951
 / Sequence 13951, Application US/10767701
 / Publication No. US20040172684A1
 / GENERAL INFORMATION:
 / APPLICANT: Kovalic, David K.
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Cao, Yongwei
 / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 / TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
 / FILE REFERENCE: 38-21(53535)B
 / CURRENT APPLICATION NUMBER: US/10/767,701
 / CURRENT FILING DATE: 2004-01-29
 / NUMBER OF SEQ ID NOS: 63128
 / SEQ ID NO 13951
 / LENGTH: 1537
 / TYPE: DNA
 / ORGANISM: Sorghum bicolor
 / FEATURE:
 / OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS2718_1
 / US-10-767-701-13951

	Query Match	76.5%;	Score 1113.4;	DB 18;	length 1597;
	Best Local Similarity	90.9%;	Pred. 0.3; 5e-304;		
	Matches 1270;	Conservative	0;	Mismatches 101;	Indels 26; Gaps 7;
QY	51	GGCGCAGACGCCCAAGACCGGAGGGGGCGGCATTCGGATCTCGAGAGCAAGGC	110		
Db	63	GTGTCGCCCGCAGAGACCCCGGGGGCGGCATTCGGATCTCGAGAGCAAGGC	122		
QY	111	CAAGGAGGCCCTTGTCGACGACGACTTCGAGCTGGCCACCGAGCTCTACACGAGGCCAT	170		
Db	123	CAAGGAGGCCCTTGTCGACGACGACTTCGAGCTGGCCCGCGAGCTCTACACCGAGGCCAT	182		
QY	171	CGACCGCGGGCGCCGACCGCGGACCTCTATGCCGACCGCGCCGAGGGCGCATCAAGCT	230		
Db	183	CGACCGGGGGCGCCGACCGCGGAACTCTACGCGACCGCGCCGAGGGCGCATCAAGCT	242		

Qy	1300	GTCTGAGTCTACTGCGGTAGCTTTTGGTGGACATA-----GGTATGCTATTATGTGGA	1355
Db	1321	GTCTGAGTCTGCTTTCGCGTAGTTTTTGGTGGACATATCATGGTATGCTATCTCTGTGGA	1380
Qy	1356	TCGACCCCGAACCATCTGTGTGATCAAGAAGCAG-CAAACTATAATGTATGGAATGCCTAT	1414
Db	1381	TC-----AACATCTGTGTGTAACAAGACAGTAAACTATAATCTGTGGAATGCCTAT	1432
Qy	1415	TCCTTTTGGTCTAAAAA	1431
Db	1433	TCCTTTTGGTCTAAAGA	1449

RESULT 7

```

US-10-425-114-25845
/ Sequence 25845, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jiongong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Kreen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 25845
/ LENGTH: 1361
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURES:
/ OTHER INFORMATION: Clone ID: LIB3960-013-B4_FLI
US-10-425-114-25845

```

Query Match	72.0%	Score 1047	DB 17	Length 1361
Best Local Similarity	92.3%	Pred. No. 21e-285		
Matches 1125	Conservative 0	Mismatches 90	Indels. 4	Gaps 2
54	GCAGACGCCCAAGCCCGAAGGGCGCCATGCGCGCTCGGATCTGTGGAGAGCAAGCCCAA	113		
71	GCAGACGCCAGAGCCGGAGGAGCGCATGGCGGCTCGGATCTGTGGAGCAAGCCCAA	130		
114	GGAGGCTTCTGTGCAGACGACATTCGAGCTGGCCACCGAGCTCTACGCCAGGCCCATCGA	173		
131	GGAGGCTTCTGTGCAGACGACATTCGAGCTGGCCACCGAGCTCTACGCCAGGCCCATCGA	190		
174	CGCGGGCGCCCAAGCCCGGCGACCTCTATGCCGACCGCGCCAGGCGCACATCTAGAGCTCGG	233		
191	CGCGGGCGCCGACCTCTCTACGCCGACCGCGCCAGGCGCACATCTAGAGCTCGG	250		
234	CAACTACATGAGGCTGTGGCGGATCTTAACAAAGCAATTGAGTCTTGATCTCTATGATGCA	293		
251	CAACTACATGAGGCTGTGGCAGATCTTAACAAAGCAATTGAGTCTTGATCTCTATGATGCA	310		
294	TAAAGCTTACTACCGGAAAGGTGCTGCATGCAATTAAGCTTGAAGAATACCAAACTGCAAA	353		
311	TAAAGCTTACTACCGGAAAGGTGCTGCATGCAATTAAGCTTGAAGAATACCAAACTGCAAA	370		
354	GGCTGCTTGTAGTTGGGTTCTTCTATGCAATCAGGCGGATTCAGAGTTTGTCTGCTATT	413		
371	GGCTGCTTGTAGTTAGGTTCTTCTATGCAATCAGGCGGATTCAGAGTTTGTCTGCTATT	430		
414	GAAGGAATGTGATGAGCGCATCGCTGAGGAATCTAGCCAGGCCACAGTAAGAATGTGGA	473		
431	GAAGGAATGTGATGAGTGCAATTCGCTGAGGAATCTAGCCAGGCCACAGTAAGAATGTGGA	490		
474	GGCTACTGTGGCTGCTACTATTGAGGACAAGGAGATTTCAAAATATGAGGAATCAACC	533		
491	GGCTCTGTAGTGCTACTATTGAGGACAAGGAGATTTGCAAAATATGAGTAATCAACC	550		

RESULT 8

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US-10-425-114-22598
; Sequence 22598, Application US/10425114
; Publication NO. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 22598
; LENGTH: 1490

```

/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB3591-005-B5_FLI
US-10-425-114-22598

Query Match 72.0%; Score 1047; DB 17; Length 1490;
Best Local Similarity 92.3%; Pred. No. 2.2e-285;
Matches 1125; Conservative 0; Mismatches 90; Indels 4; Gaps 2;

QY 54 GCAGAGCCCAAGCGGAGGCGCGCATGGCGCGTGGATCTGGAGAGCAAGGCCAA 113
DB 139 GCAGAGCCCAAGCGGAGGCGCGCATGGCGCGTGGATCTGGAGAGCAAGGCCAA 198
QY 114 GGAGGCGCTTGGTGGAGCAGCACTTTCGAGCTGGCCACCGAGCTCTACAGCCAGCCATCGA 173
DB 199 GGAGGCGCTTGGTGGAGCAGCACTTTCGAGCTGGCCACCGAGCTCTACAGCCAGCCATCGA 258
QY 174 CGCGGCGCCCGCACCGCGCACTCTATGCGGACCGCGCCAGCGGCACATCAAGCTCGG 233
DB 259 CGCGGCGCCCGCACCGCGCACTCTATGCGGACCGCGCCAGCGGCACATCAAGCTCGG 318
QY 234 CAACTACACTGAGCTGTGGCGGATGCTAAACAGCAATTGAGCTTGATCTTATGATGA 293
DB 319 CAACTACACTGAGCTGTGGCGGATGCTAAACAGCAATTGAGCTTGATCTTATGATGA 378
QY 294 TAAAGCTTACTACCGGAAAGGCTGCTGCATGCATTAAAGCTTGAAGAAATACCAACTGCATA 353
DB 379 TAAAGCTTACTACCGGAAAGGCTGCTGCATGCATTAAAGCTTGAAGAAATACCAACTGCATA 438
QY 354 GGCTGCTTTGAGTGGGTTCTTCTATGATCATGAGCGGATCAAGTTGCTCGTCTATT 413
DB 439 GGCTGCTTTGAGTGGGTTCTTCTATGATCATGAGCGGATCAAGTTGCTCGTCTATT 498
QY 414 GAAGGATGTGATGAGCGCATCTGAGGAGTCTAGCCAGGCGCCAGTAAGAAATGTGA 473
DB 499 GAAGGATGTGATGAGCGCATCTGAGGAGTCTAGCCAGGCGCCAGTAAGAAATGTGA 558
QY 474 GGCTGCTTGGCTGCTACTATTGAGGAGCAAGGAGGATTTACAAATATGAGAAATACACC 533
DB 559 GGCTGCTTGGCTGCTACTATTGAGGAGCAAGGAGGATTTACAAATATGAGAAATACACC 618
QY 534 ACAGTATAGAACCCCAAGCAACCAAAATACAGCGCATGACTACAAACAGTGGCCAC 593
DB 619 GCCAGTGGTAGAACCCCAAGCAACCAAAATATAGGCATGACTACTACAAACAGTGGCCAC 678
QY 594 AGAAGTGGTACTGACATATTGCTAAGGGTGTCTGCTGATGATGCTAGTCAATTGATT 653
DB 679 AGAAGTGGTCTCAATATATGCTAAGGGTGTCTGCTGATGATGCTAGTCAATTGATT 738
QY 654 TGGTGAACAGATGTTGAGTGTATCCATTGAAGTTCTGTTGAGAAACCATACCAATTTCA 713
DB 739 TGGTGAACAGATGTTGAGTGTATCCATTGAAGTACTGTTGAGAAACCGTACCAATTTCA 798
QY 714 GCCCGCTGTGTTTCTAAGATTATCCCTGAGAAATGCAAAATATCAAGTCTTATCCACAA 773
DB 799 GCCCGCTGTGTTTCTAAGATTATCCCTGAGAAATGCAAAATATCAAGTCTTATCCACAA 858
QY 774 GGTGAATACCGCTCCGAAAGCTGAGCGAGTGCATGAGCAACCTCGGATTTATAGTGG 833
DB 859 GGTGGAATACCGCTCCGAAAGCTGAGCGAGTGCATGAGCAACCTCGGATTTATAGTGG 918
QY 834 AAGACCAAGAGCTGTCCCAAGAGATAAGCACCCAGCTGAAACAGCCCAAGACCTTC 893
DB 919 AAGACCAAGAGCTGTCCCAAGAGATAAGCACCCAGCTGAAACAGCCCAAGACCTTC 978
QY 894 ATACCCATCTTCAAAGCGGAAAAAGACTGGGATAAATCTGGAAGCTGAAGTCAAAAAGGA 953
DB 979 ATACCCATCTTCAAAGTCAAAAAGGACTGGGATAAATCTGGAAGCTGAAGTCAAAAAGGA 1038
QY 954 GGAGAGGAGAAAAAATTGATGCTGATGCTGCAATGCAAAATCTTCCGCTGACATCTA 1013
DB 1039 GGAGAGGAGAAAAAATTGATGCTGATGCTGCAATGCAAAATCTTCCGCTGATCTA 1098

QY 1014 CAAGATGCTGATGAAGATATGCGAGGGCCATGATGAAGTCAATTCGTGGAATCAATGG 1073
DB 1099 CAAGATGCTGATGAAGATATGCGAGGGCCATGGAACAGTCAATTCAGGGAATCTAATGG 1158
QY 1074 CACTGTTCTCTCAACCAATTGGAAAGATGCTGAGCAAAAGAGGTAGAAAGGAGGAGCCGCC 1133
DB 1159 TACCGTTCTCTCAACCAATTGGAAAGATGTTGATCAAGAGCGGTGGAAGCGAGCCCTCC 1218
QY 1134 TGATGGTATGAGCTCAAGAGTGGGAATATCTAAAGTTTGGACTGCGCCCTCTTTGTAAA 1193
DB 1219 TGATGGTATGAGCTCAAGAGTGGGAATATCTAAAGTTTGGACTGCGCC--CTCTGTAAA 1276
QY 1194 TCCAGCTCTTGAAGAACTATGACCTAATCTGCCCCACCA--TAGTGCCATGAGCTTGT 1251
DB 1277 TCCAGCTCTTGAAGTATGACCTAGTTCTGTGCCACCAATTTGGTGTCTGTAAGTTTGGTT 1336
QY 1252 GGTAAAGTCTCTGCTTTTG 1270
DB 1337 AAGTGTGTGTGTTTGG 1355

RESULT 9

US-10-425-115-18041
; Sequence 18041, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 18041
; LENGTH: 1519
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_116456C.1
US-10-425-115-18041

Query Match 71.9%; Score 1046; DB 18; Length 1519;
Best Local Similarity 92.3%; Pred. No. 4.3e-285;
Matches 1124; Conservative 0; Mismatches 90; Indels 4; Gaps 2;

QY 54 GCAGAGCCCAAGCGGAGGCGCCATGGCGCGTCCGATCTGGAGAGCAAGGCCAA 113
DB 139 GCAGAGCCCAAGCGGAGGCGCCATGGCGCGTCCGATCTGGAGAGCAAGGCCAA 198
QY 114 GGAGGCGCTTGGTGGAGCAGCACTTTCGAGCTGGCCACCGAGCTCTACAGCCAGGCCATCGA 173
DB 199 GGAGGCGCTTGGTGGAGCAGCACTTTCGAGCTGGCCACCGAGCTCTACAGCCAGGCCATCGA 258
QY 174 CGCGGCGCCCGCACCGCGCACTCTATGCGGACCGCGCCAGCGGCACATCAAGCTCGG 233
DB 259 CGCGGCGCCCGCACCGCACTCTATGCGGACCGCGCCAGCGGCACATCAAGCTCGG 318
QY 234 CAACTACACTGAGCTGTGGCGGATGCTAAACAGCAATTGAGCTTGATCTTATGATGA 293
DB 319 CAACTACACTGAGCTGTGGCGGATGCTAAACAGCAATTGAGCTTGATCTTATGATGA 378
QY 294 TAAAGCTTACTACCGGAAAGGCTGCTGCATGCAATTAAGCTTGAAGAAATACCAACTGCATA 353
DB 379 TAAAGCTTACTACCGGAAAGGCTGCTGCATGCAATTAAGCTTGAAGAAATACCAACTGCATA 438
QY 354 GGCTGCTCTTGAAGTTGGGTTCTTCTTATGATCATGAGCGGATTCAGGTTTGTGCTCTATT 413
DB 439 GGCTGCTCTTGAAGTTGGGTTCTTCTTATGATCATGAGCGGATTCAGGTTTGTGCTCTATT 498

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QY 414 GAAGGAATGTGATGAGCGCATCGCTGAGGAATCTAGCCAGGACCAGTAAGAATGTTGA 473
DB 499 GAAGGAATGTGATGAGCGCATCGCTGAGGAATCTAGCCAGGACCAGTAAGAATGTTGA 558
QY 474 GCTACTGTGGCTGCTACTATTGAGGACAGGAGGATTTCAAAATATGGAGATACACC 533
DB 559 GGTCTCTGTAGCTGCTACTATTGAGGACAGGAGGATGTCGAATATGGATATACACC 618
QY 534 ACCAGTGATAGAACCCCAAGCAACCAACCAATATACAGGATGACTACTCAACAGTGCCAC 593
DB 619 GCCAGTGATAGAACCCCAAGCAACCAACCAATATATAGGATGACTACTCAACAGTGCCAC 678
QY 594 AGAAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 653
DB 679 AGAAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 738
QY 654 TGGTGAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 713
DB 739 TGGTGAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 798
QY 714 GCCCGCTGCTGTTTCTTAAGATTATCCCTGAGAAATGCAATATCAAGTCTTTATCCACAA 773
DB 799 GCCCGCTGCTGTTTCTTAAGATTATCCCTGAGAAATGCAATATCAAGTCTTTATCCACAA 858
QY 774 GGTGGAATATAGCGCTTGCACCAAGCTGAGCAGTGACATGACACCTGATGATGATGATGAT 833
DB 859 GGTGGAATATAGCGCTTGCACCAAGCTGAGCAGTGACATGACACCTGATGATGATGATGAT 918
QY 834 AAGACCAAGATGTTTCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 893
DB 919 AAGACCAAGATGTTTCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 978
QY 894 ATACCCATCTTCAAGGCGGAAAGAAAGCTGGGATATAAAGCTGGAAGTGAAGTGAAGTGA 953
DB 979 ATACCCATCTTCAAGGCGGAAAGAAAGCTGGGATATAAAGCTGGAAGTGAAGTGAAGTGA 1038
QY 954 GGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1013
DB 1039 GGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1098
QY 1014 CAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1073
DB 1099 CAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1158
QY 1074 CACTGTTCTCTCAACCAATGGAAGATGTTGAGCAAGATGTTGAGCAAGATGTTGAGCAAG 1133
DB 1159 TACCGTTCTCTCAACCAATGGAAGATGTTGAGCAAGATGTTGAGCAAGATGTTGAGCAAG 1218
QY 1134 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1193
DB 1219 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1276
QY 1194 TCCAGTCTTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1251
DB 1277 TCCAGTCTTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1336
QY 1252 GGTAAAGTCTGCTGTTTT 1269
DB 1337 AAGTGTGTGTGTTTTT 1354

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RESULT 10

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US-10-739-930-4858/c
/ Sequence 4858, Application US/10739930
/ Publication No. US20040216190A1
/ GENERAL INFORMATION:
/ APPLICANT: Kovalic, David K.
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
/ TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
/ FILE REFERENCE: 38-21(53377)B
/ CURRENT APPLICATION NUMBER: US/10/739,930
/ CURRENT FILING DATE: 2003-12-18
/ NUMBER OF SEQ ID NOS: 11088

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/ SEQ ID NO 4858
/ LENGTH: 2471
/ TYPE: DNA
/ ORGANISM: Triticum aestivum
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(2471)
/ OTHER INFORMATION: unsure at all n locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: TRIAB-23APR03-CLUSTER396_1
US-10-739-930-4858

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Query Match      51.8%; Score 753; DB 18; Length 2471;
Best Local Similarity 79.3%; Pred. No. 5.6e-202;
Matches 938; Conservative 0; Mismatches 200; Indels 45; Gaps 2;

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QY 61 CCCAAGCCCGAAGGGCGCCATGCGCGCTCGATCTCGAGTCTGGAGAGCAAGGCCAAGAGGCC 120
DB 2303 CTCGACGCGACATGCGCGCGCGCGCTCGATCTCGAGAGCAAGGCCAAGAGGCC 2244
QY 121 TTGCTCGACGACGACTTCGAGCTGGCCACCGAGCTCTACAGCCAGGCGCATCGAGCGCGG 180
DB 2243 TTGCTCGACGACGACTTCGAGCTGGCCACCGAGCTCTACAGCCAGGCGCATCGAGCGGG 2184
QY 181 CCGCCACCGCGGACCTCTATGCGGACCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGG 240
DB 2183 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2124
QY 241 ACTGAGGCTGTGGCGGATGCTTAACAAAGCAATTTGAGCTTTCATCTATGATGCAATAAGCT 300
DB 2123 ACTGAGGCTGTAGCTGATGCGCAACAAAGCAATTTGAGCTTTCATCTATGATGCAATAAGCA 2064
QY 301 TACTACCGGAAAGGCTGCTGATGCAATTAAGCTTGAAGATACAAATCTCAAAAGGCTGCT 360
DB 2063 TACCTTGGGAGGCGCTGCTGCTGATGCAATTAAGCTTGAAGATACAAATCTCAAAAGGCTGCT 2004
QY 361 CTGAGTGTGGGTTCTTCTTATGCAATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
DB 2003 CTGAGTGTGGGTTCTTCTTATGCAATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1944
QY 421 TGTGATGAGCGCATCGCTGAGGAACTAGCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
DB 1943 TGTGATGATGCTATGCTGAGGAGGCTAGCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1884
QY 481 GTGGCT-----GCTACTATTGAG 498
DB 1893 GTTGTTCAGCTACATCTTCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1824
QY 499 GACAGGAGGAGTTCACAAATATGAGGAATACACCCAGGCGGCGGCGGCGGCGGCGGCGGCGG 558
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QY 559 CCAAAATACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 618
DB 1763 CCAAAATACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1704
QY 619 AAGGTTGTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 678
DB 1703 AAGGTTGTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1644
QY 679 ATTGAAGTTCCTGGTGAAGAACCATACCATTTTCAGCGCGGCGGCGGCGGCGGCGGCGGCGG 738
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DB 1583 CCAGATAAGTGAAGTATGCTGTTGTTCTTCAAAAGGTTGAAATGCGCTTTCGAAAAGCT 1524
QY 799 GAGCAGTGATGAGCAACCGCTGGATTTATGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGG 858
DB 1523 GAGCAGTGATGAGCAACCGCTGGATTTATGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1467
QY 859 ATAAGCAGCGGAGCTGAAGAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 918

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 23, 2005, 03:11:06 / Search time 685.535 Seconds
(without alignments)
9617.545 Million cell updates/sec

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Perfect score: 1086
Sequence: 1 atggccggtcggtatcgga.....tcaagaagtgggaatactaa 1086

Scoring table: IDENTITY_NUC
Gapop 10.0 / Gapext 1.0

Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score-distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1084.4	99.9	1444	17	US-10-425-114-15440
2	1084.4	99.9	1450	17	US-10-425-114-25244
3	1084.4	99.9	1755	18	US-10-425-115-18040
4	988.2	91.9	1537	17	US-10-767-701-13951
5	977.6	90.0	1361	17	US-10-425-114-25845
6	977.6	90.0	1490	17	US-10-425-114-22598
7	977.6	90.0	1519	18	US-10-425-115-18041
8	862	79.4	1649	17	US-10-425-114-24871
9	862	79.4	1706	18	US-10-425-115-18039
10	736.6	67.8	2471	18	US-10-739-930-4858
11	698.2	64.3	1569	18	US-10-437-963-37229

12	490	45.1	571	16	US-10-074-473-2	Sequence 2, Appli
13	476.8	43.9	1691	17	US-10-424-599-65699	Sequence 65699, A
14	474.4	43.7	1598	17	US-10-424-599-81927	Sequence 81927, A
15	416.6	38.4	483	17	US-10-424-599-118531	Sequence 118531, A
16	332.8	30.6	1674	17	US-10-424-599-98272	Sequence 98272, A
17	286	26.3	287	9	US-09-294-093B-571	Sequence 571, App
18	243.4	22.4	1029	17	US-10-424-599-81933	Sequence 81933, A
19	221.8	20.4	585	18	US-10-021-323-2492	Sequence 2492, Ap
20	217.8	20.1	534	18	US-10-021-323-14417	Sequence 14417, A
21	216.4	19.9	272	9	US-09-294-093B-4704	Sequence 4704, Ap
22	201.6	18.6	851	17	US-10-424-599-75856	Sequence 75856, A
23	194.4	17.9	528	18	US-10-021-323-14351	Sequence 14351, A
24	183.6	16.9	573	18	US-10-021-323-2546	Sequence 2546, Ap
25	182.8	16.8	275	18	US-10-425-115-60448	Sequence 60448, A
26	180.6	16.6	656	17	US-10-424-599-98270	Sequence 98270, A
27	175.4	16.2	523	18	US-10-021-323-15961	Sequence 15961, A
28	156.4	14.4	1264	17	US-10-264-049-918	Sequence 918, App
29	156.4	14.4	1366	16	US-10-287-218-33	Sequence 33, Appl
30	156.4	14.4	1366	18	US-10-474-291-33	Sequence 33, Appl
31	156.4	14.4	1555	18	US-10-335-053-99	Sequence 99, Appl
32	156.4	14.4	1776	18	US-10-357-930-22330	Sequence 22330, A
33	156.4	14.4	1776	18	US-10-357-930-28174	Sequence 28174, A
34	156.4	14.4	2053	10	US-09-983-802-45	Sequence 45, Appl
35	156.4	14.4	2053	10	US-09-984-490-45	Sequence 45, Appl
36	156.4	14.4	2053	11	US-09-973-278-82	Sequence 82, Appl
37	148.6	13.7	291	9	US-09-294-093B-3135	Sequence 3135, Ap
38	141.4	13.0	409	9	US-09-770-423-621	Sequence 621, App
39	129.2	11.9	481	10	US-09-770-961-929	Sequence 929, App
40	125	11.5	388	16	US-10-074-473-3	Sequence 3, Appl1
41	106.8	9.8	479	17	US-10-424-599-25942	Sequence 25942, A
42	106	9.8	432	17	US-10-424-599-49836	Sequence 49836, A
43	94.4	8.7	317	17	US-10-424-599-41142	Sequence 41142, A
44	93.2	8.6	672	17	US-10-260-238-1154	Sequence 1154, Ap
45	93.2	8.6	672	18	US-10-437-963-43909	Sequence 43909, A

ALIGNMENTS

RESULT 1
US-10-425-114-15440
; Sequence 15440, Application US/10425114
; Publication No: US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 15440
; LENGTH: 1444
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3059-061-D10_FLI
US-10-425-114-15440

Query Match 99.9% Score 1084.4; DB 17; Length 1444;
Best Local Similarity 99.9%; Pred. No. 5.3e-313;
Matches 1085; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGCCCGCGTCGGATCTGGAGACCAAGGCCAAGGAGCGCTTCGTCGACGACGACTTCGAG 60
Db 83 ATGCCCGCGTCGGATCTGGAGACCAAGGCCAAGGAGCGCTTCGTCGACGACGACTTCGAG 142
Qy 61 CTGGCCACCGAGCTCTACAGCCAGGCCATCGACGCCGGGCCCGCCGACCTCTAT 120

Db	143	CTGCGCCACCGAGCTCTACAGCGAGCCATCGACGCCGGGCCGCAACGCGGAGCTCTAT	202
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Db	203	GCCGACCGCGCCACGAGCGCACATCAAGCTCGGCAACTACACTGAGGCTGTGGCGGATGCT	262
Qy	181	AACAAAGCAATTGAGCTTGATTCCTATGATGTCATAAAGCTTACTACCGGAAAGTGCTGCA	240
Db	263	AACAAAGCAATTGAGCTTGATTCCTATGATGTCATAAAGCTTACTACCGGAAAGTGCTGCA	322
Qy	241	TGCATTAAAGCTTGAAGATAACCAACTGCAAGGCTGCTCTGAGTTGGGTTCTTCTTAT	300
Db	323	TGCATTAAAGCTTGAAGATAACCAACTGCAAGGCTGCTCTGAGTTGGGTTCTTCTTAT	382
Qy	301	GCATCAGGCGATTCAAGGTTTGCTCGTCTATTGAAGGAATGTGATGAGCGCATCGCTGAG	360
Db	383	GCATCAGGCGATTCAAGGTTTGCTCGTCTATTGAAGGAATGTGATGAGCGCATCGCTGAG	442
Qy	361	GAATCTAGCAGGACACAGTAAAGATGTTGAGGCTACTGTGGCTGCTACTATTGAGGAC	420
Db	443	GAATCTAGCAGGACACAGTAAAGATGTTGAGGCTACTGTGGCTGCTACTATTGAGGAC	502
Qy	421	AAGGAGGATTTCACAAATATGGGAATACACACAGTGTAGAACCCCCCAAGCAACCA	480
Db	503	AAGGAGGATTTCACAAATATGGGAATACACACAGTGTAGAACCCCCCAAGCAACCA	562
Qy	481	AAATACAGGCACTGACTACTACAAAGTGCACAGAGTGGTACTGACAAATATTGCTTAAG	540
Db	563	AAATACAGGCACTGACTACTACAAAGTGCACAGAGTGGTACTGACAAATATTGCTTAAG	622
Qy	541	GGTGTTCTGCTGATAGTGTAGTCAATTTGGTGAAAGAGTGTGAGTGATTCATT	600
Db	623	GGTGTTCTGCTGATAGTGTAGTCAATTTGGTGAAAGAGTGTGAGTGATTCATT	682
Qy	601	GAAGTTCCTGGTGAGAACCATACCATTTTCAGCCCCGTCTGTTTTCTTAAGATTATCCCT	660
Db	683	GAAGTTCCTGGTGAGAACCATACCATTTTCAGCCCCGTCTGTTTTCTTAAGATTATCCCT	742
Qy	661	GAGAAATGCAAAATATCAAGTCTTATCCACCAAGGTTGAAATACGCCTTGCMAAGCTGAG	720
Db	743	GAGAAATGCAAAATATCAAGTCTTATCCACCAAGGTTGAAATACGCCTTGCMAAGCTGAG	802
Qy	721	CAGGTGATATGGACAAACCTGGATTATAGTGGAGACCAAAGACTGTTTCCCGAAGATA	780
Db	803	CAGGTGATATGGACAAACCTGGATTATAGTGGAGACCAAAGACTGTTTCCCGAAGATA	862
Qy	781	AGCACGCCAGCTGAAACAGCCCCAGACCTTCATACCCATCTTCAAAGGCGAAAAAGAC	840
Db	863	AGCACGCCAGCTGAAACAGCCCCAGACCTTCATACCCATCTTCAAAGGCGAAAAAGAC	922
Qy	841	TGGGATTAACCTGGAGCTGAAGTCAAAAAGGAGAGAAAGAAAACCTTGATGGTGAT	900
Db	923	TGGGATTAACCTGGAGCTGAAGTCAAAAAGGAGAGAAAGAAAACCTTGATGGTGAT	982
Qy	901	GCTGCATTGAACAAATTCCTCCGTCACATCTACAAAGGATCTGATGAAGATATGCGGAGG	960
Db	983	GCTGCATTGAACAAATTCCTCCGTCACATCTACAAAGGATCTGATGAAGATATGCGGAGG	1042
Qy	961	GCCATGATGAAGTCATTCTGGTGGAAATCAAAATGGCACTGTTCTCTCAACCAATTGGAAGAT	1020
Db	1043	GCCATGATGAAGTCATTCTGGTGGAAATCAAAATGGCACTGTTCTCTCAACCAATTGGAAGAT	1102
Qy	1021	GTGCGAGCAAAAGGTAGAGGAGGCCCCCTTGATGGTATGGAGCTCAAGAAAGTGGGAA	1080
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RESULT 2

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US-10-425-114-25244
; Sequence 25244, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 25244
; LENGTH: 1450
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3732-024-C2_FLI
US-10-425-114-25244

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Query Match	99.9%	Score 1084.4	DB 17	Length 1450
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Db	89	ATGGCCGCTCGGATCTGGAGACAAGGCCAAGGAGGCCTTCGTCGACGACGACTTCGAG	148	
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Db	149	CTGGCCACCGAGCTCTACAGCCAGGCGCATCGAGCGCGGGCCCGCCACCGCCGACCTCTAT	208	
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Db	209	GCCGACCGGCCCCAGGCGGCACATCAAGCTGGCAACTACACTGAGGCTGTGGCGGATGCT	268	
Qy	181	AACAAAGCAATTGAGCTTGATCCTATGATGCTATAAAGCTTACTACCGGAAGGTGCTGCA	240	
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Qy	241	TGCATTAAAGCTTCAAGAATACCAAACTGCAAAAGGCTGCTCTTCAGTTGGGTTCTTCTTAT	300	
Db	329	TGCATTAAAGCTTCAAGAATACCAAACTGCAAAAGGCTGCTCTTCAGTTGGGTTCTTCTTAT	388	
Qy	301	GCATCAGGCGAATCAAGGTTTGCTCGTCTATTGAAGGAATGTGATGAGCGCATCGCTGAG	360	
Db	389	GCATCAGGCGAATCAAGGTTTGCTCGTCTATTGAAGGAATGTGATGAGCGCATCGCTGAG	448	
Qy	361	GAATCTAGCGAGCCACAGTAAAGAATGTTGAGGCTACTGTGTGCTGCTACTATTGAGGAC	420	
Db	449	GAATCTAGCGAGCCACAGTAAAGAATGTTGAGGCTACTGTGTGCTGCTACTATTGAGGAC	508	
Qy	421	AAGGAGGATTCACAATATGGAGAATACACCAACAGTGATAGAACCCCAAGCAAAACCA	480	
Db	509	AAGGAGGATTCACAATATGGAGAATACACCAACAGTGATAGAACCCCAAGCAAAACCA	568	
Qy	481	AAATACAGGCATGACTACTACACAGTGGCCACAGAAGTGCTATCTGACAAATATTGCTAAG	540	
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Db 869 AGCAGCGCAGTGAACAGCCCAAGACCTTCATACCCATCTTCAAGGCGGAAAAAGAC 928
Qy 841 TGGGATAAATCGGAGCTGAAGTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db 929 TGGGATAAATCGGAGCTGAAGTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 988
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Db 989 GCTGCATTGAACAAATCTTCGTCGACATCTCAAGAGGATGCTGATGAAGATATGCGGAGG 1048
Qy 961 GCCATGATGAAGTCAATTCGTGGAATCAAAATGGCACTGTTCTCAACCAATTGGAAGAT 1020
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Qy 1021 GTTGAGCAAGAGGATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
Db 1109 GTTGAGCAAGAGGATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1168
Qy 1081 TACTAA 1086
Db 1169 TACTAA 1174

RESULT 3

US-10-425-115-18040
; Sequence 18040, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 18040
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_116455C.1
US-10-425-115-18040

Query Match 99.9%; Score 1084.4; DB 18; Length 1755;
Best Local Similarity 99.9%; Pred. No. 5.8e-313;
Matches 1085; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGGCCGCGTCGATCTGAGAGCAAGGCAAGAGGAGGCTTCGTCGAGCGACTTCGAG 60
Db 252 ATGGCCGCGTCGATCTGAGAGCAAGGCAAGAGGAGGCTTCGTCGAGCGACTTCGAG 311
Qy 61 CTGGCCAGCGAGCTTACAGCCAGGCTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTAT 120
Db 312 CTGGCCAGCGAGCTTACAGCCAGGCTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTAT 371
Qy 121 CGCGACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 180
Db 372 CGCGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 431
Qy 181 AACAAAGCAATGAGCTTGATCTTATGATGCAATGAAGCTTACTACCGGAAAGGTCGTGCA 240

RESULT 4

US-10-767-701-13951
; Sequence 13951, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

Db 432 AACAAAGCAATGAGCTTGATCTCTATGATGCAATAAGCTTACTACCGGAAAGGTCGTCA 491
Qy 241 TGCATTAAGCTTGAAGAAATACAAACTGCAAAAGGCTGCTCTTGAGTTGGGTTCTTTTAT 300
Db 492 TGCATTAAGCTTGAAGAAATACAAACTGCAAAAGGCTGCTCTTGAGTTGGGTTCTTTTAT 551
Qy 301 GCATCAGCGGATTCAGGTTTGCTCGTCTATTGAAGGAAATGATGAGCGCATCGCTGAG 360
Db 552 GCATCAGCGGATTCAGGTTTGCTCGTCTATTGAAGGAAATGATGAGCGCATCGCTGAG 611
Qy 361 GAATCTAGCAGGCAACAGTAAGAAATGTCAGGCTACTGTTGGGCTGCTACTATTGAGGAC 420
Db 612 GAATCTAGCAGGCAACAGTAAGAAATGTCAGGCTACTGTTGGGCTGCTACTATTGAGGAC 671
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Db 672 AAGGAGGATTTTCAAAAATATGAGAGATAACACACAGTATAGAACCCCAAGCAAAACA 731
Qy 481 AAATACAGGCAATGACTACTACACAGTGCACAGAGTGGTACTGACAAATATTTGCTAAG 540
Db 732 AAATACAGGCAATGACTACTACACAGTGCACAGAGTGGTACTGACAAATATTTGCTAAG 791
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Db 792 GGTGTTCTGCTGATAGTGTAGTCAATTGTTTGTGAACAGATGTTTGTGAGTGTATCCATT 851
Qy 601 GAAGTTCTGCTGAGAAACCAATACCAATTTTTCAGGCCGCTGCTGTTTTCATGATATTCCT 660
Db 852 GAAGTTCTGCTGAGAAACCAATACCAATTTTTCAGGCCGCTGCTGTTTTCATGATATTCCT 911
Qy 661 GAGAAATGCAAAATATCAAGTCTTATCCACCAAGGTTGAAATACGCTTTCGCAAAAGCTGAG 720
Db 912 GAGAAATGCAAAATATCAAGTCTTATCCACCAAGGTCGAAATACGCTTTCGCAAAAGCTGAG 971
Qy 721 CAGGTGACATGGACCAACCTCGATTATAGTGAAGACCAAGACCTGTTCCCAAGAGATA 780
Db 972 CAGGTGACATGGACCAACCTCGATTATAGTGAAGACCAAGACCTGTTCCCAAGAGATA 1031
Qy 781 AGCAGCGCAGCTGAAACAGCCCAAGACCTTTCATACCCATCTTCAAAAGCGGAAAAAGAC 840
Db 1032 AGCAGCGCAGCTGAAACAGCCCAAGACCTTTCATACCCATCTTCAAAAGCGGAAAAAGAC 1091
Qy 841 TGGGATAAATCGGAGCTGAAGTCAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 1092 TGGGATAAATCGGAGCTGAAGTCAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1151
Qy 901 GCTGCATTGAACAAATCTTCGTCGACATCTCAAGAGGATGCTGATGAAGATATGCGGAGG 960
Db 1152 GCTGCATTGAACAAATCTTCGTCGACATCTCAAGAGGATGCTGATGAAGATATGCGGAGG 1211
Qy 961 GCCATGATGAAGTCAATTCGTGGAATCAAAATGGCACTGTTCTCTCAACCAATTGGAAGAT 1020
Db 1212 GCCATGATGAAGTCAATTCGTGGAATCAAAATGGCACTGTTCTCTCAACCAATTGGAAGAT 1271
Qy 1021 GTTGAGCAAGAGAGGATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
Db 1272 GTTGAGCAAGAGAGGATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1331
Qy 1081 TACTAA 1086
Db 1332 TACTAA 1337

361 GAATCTAGCCAGGACCAAGTAAGAAATGTTGAGGCTACTGTGGCTGCTACTATTGAGGAC 420
 459 GAATCTAGCCAGGACCAAGTAAGAAATGTTGAGGCTACTGTGGCTGCTACTATTGAGGAC 518
 421 AAGGAGATTTTCAAAATATGGAGAAATACACCAAGCTAGATAGAACCCCAAGCAACCA 480
 519 AAGGAGATGTCGCAAAATATGGAGAAATACACCAAGCTAGATAGAACCCCAAGCAACCT 578
 481 AATATACAGGATGACTACTACCAAGTGCACAGAGTGGTACTGACAAATATTGCTAAG 540
 579 AATATAGGATGACTACTACCAAGTGCACAGAGTGGTACTGACAAATATTGCTAAG 638
 541 GGTGTTCTGCTGATAGTAGTCAATGATTTTGGTGAACAGATGTTGAGTGATCCATT 600
 639 GGTGTTCTGCTGATAGTAGTCAATGATTTTGGTGAACAGATGTTGAGTGATCCATT 698
 601 GAAGTTCTGGTGAAGAACCATACCAATTTTCCAGCCCGCTGTTTCTTAGATTTATCCCT 660
 699 GAAGTTCTGGTGAAGAACCATACCAATTTTCCAGCCCGCTGTTTCTTAGATTTATCCCT 758
 661 GAGAAATGCAAAATATCAAGTCTTATCCACCAAGGTTGAAATACGCCCTTGCACCAAGCTGAG 720
 759 GAGAAATGCAAGTATCAAGTCTTATCCACCAAGGTTGAAATACGCCCTTGCACCAAGCTGAG 818
 721 CAGTGACATGGACCAACCTGGATTATAGTGAAGACCAAGACTGTTCCCAAGAGATA 780
 819 CAGTGACATGGACCAACCTGGATTATAGTGAAGACCAAGACTGTTCCCAAGAGATA 878
 781 AGCAGCAGCTGAAACAGCCCAAGACTTTCATACCCATCTTCAAGGGGCAAAAGAC 840
 879 AGCAGCAGCTGAAACAGCCCAAGACTTTCATACCCATCTTCAAGGGGCAAAAGAC 938
 841 TGGGATAAATCGGAAGCTGAAGTCAAAAGAGGAGAGGAAGAAACCTTGTATGTTGAT 900
 939 TGGGATAAATCGGAAGCTGAAGTCAAAAGAGGAGAGGAAGAAACCTTGTATGTTGAT 998
 901 GCTGATTTGAACAAATCTTCCGCTGACATCTACCAAGGATGCTGATGAAGATATCGGAGG 960
 999 GCTGATTTGAACAAATCTTCCGCTGACATCTACCAAGGATGCTGATGAAGATATCGGAGG 1058
 961 GCCATGATGAAGTCAATTCGTTGGAATCAAAATGGCACTGTTCTCTCAACCAATTTGAAAGAT 1020
 1059 GCCATGATGAAGTCAATTCGTTGGAATCAAAATGGCACTGTTCTCTCAACCAATTTGAAAGAT 1118
 1021 GTTGGACCAAGAGTGAAGGAGGAGCCCTGATGATGATGAGCTCAAGAGTGGGAA 1080
 1119 GTTGGACCAAGAGTGAAGGAGGAGCCCTGATGATGATGAGCTCAAGAGTGGGAA 1178

RESULT 6

US-10-425-114-22598
 ; Sequence 22598, Application US/10425114
 ; Publication No. US2004003488A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 22598
 ; LENGTH: 1490
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3591-005-E5_FLI
 US-10-425-114-22598

Query Match 90.0%; Score 977.6; DB 17; Length 1490;
 Best Local Similarity 94.1%; Pred. No. 4.6e-281;
 Matches 1016; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy	1	ATGCGCGCGTGGATCTGGAGAGCAAGGCCAGGAGGCTTCTGTCGACGACGACTTCGAG	60
Db	167	ATGCGCGCGTGGATCTGGAGAGCAAGGCCAGGAGGCTTCTGTCGACGACGACTTCGAG	226
Qy	61	CTGCGCACCGAGCTCTACAGCCAGGCGCATCGACGCGGGCCCGCCACCGCGACTCTAT	120
Db	227	CTGCGCGCGGAACTCTACAGCGAGCCATCGACGCGGGCCCGCCACTGCGGATCTCTAC	286
Qy	121	GCCGACCGCGCCGAGCGGCAATCAAGCTCGGCAACTACCTAGAGCTGTGGCGGATGCT	180
Db	287	GCCGACCGCGCCGAGCGGCAATCAAGCTCGGCAACTACCTAGAGCTGTGGCGGATGCT	346
Qy	181	AACAAAGCAATTGAGCTTGTATCTATGATGATCAATAAGCTTACTACCGGAAAGGTGCTGCA	240
Db	347	AACAAAGCAATTGAGCTTGTATCTATGATGATCAATAAGCTTACTACCGGAAAGGTGCTGCA	406
Qy	241	TGCAATTAAGCTTGAAGAAATACCAAACTGCAAAAGGCTGCTCTTGAGTTGGGTTCCTTAT	300
Db	407	TGCAATTAAGCTTGAAGAAATACCAAACTGCAAAAGGCTGCTCTTGAGTTGGGTTCCTTAT	466
Qy	301	GCATCAGGCGGATCAAGGTTTGTCTGCTTATGAAGAAATGTGATGAGCGCATCGCTGAG	360
Db	467	GCATCAGGCGGATCAAGGTTTGTCTGCTTATGAAGAAATGTGATGAGCGCATCGCTGAG	526
Qy	361	GAATCTAGCCAGGACCAAGTAAGAAATGTTGAGGCTACTGTGGCTGCTACTATTGAGGAC	420
Db	527	GAATCTAGCCAGGACCAAGTAAGAAATGTTGAGGCTACTGTGGCTGCTACTATTGAGGAC	586
Qy	421	AAGGAGATTTTCAAAATATGGAGAAATACACCAAGTGTAGTAAGACCCCAAGCAACCA	480
Db	587	AAGGAGATTTTCAAAATATGGAGAAATACACCAAGTGTAGTAAGACCCCAAGCAACCA	646
Qy	481	AAATACAGGCACTGACTACTACCAAGTGTAGTAAGTGTGTAAGTGTGTAAGTGTGTAAG	540
Db	647	AAATACAGGCACTGACTACTACCAAGTGTAGTAAGTGTGTAAGTGTGTAAGTGTGTAAG	706
Qy	541	GGTGTTCCTGCTGATAGTGTAGTCAATGATTTTGGTGAACAGATGTTGAGTGTATCCATT	600
Db	707	GGTGTTCCTGCTGATAGTGTAGTCAATGATTTTGGTGAACAGATGTTGAGTGTATCCATT	766
Qy	601	GAAGTTCCTGCTGAGAAACCATACCATTTTTCAGCCCGCTGTTTCTTAAGATTTATCCCT	660
Db	767	GAAGTTCCTGCTGAGAAACCATACCATTTTTCAGCCCGCTGTTTCTTAAGATTTATCCCT	826
Qy	661	GAGAAATGCAAAATATCAAGTCTTATCCCAAGGTTGAAATACGCTTGCACCAAGCTGAG	720
Db	827	GAGAAATGCAAGTATCAAGTCTTATCCCAAGGTTGAAATACGCTTGCACCAAGCTGAG	886
Qy	721	CAGTGATGAGCAACCTCTGATTTATAGTGAAGACCAAGACTGTTCCCAAGAGATA	780
Db	887	CAGTGATGAGCAACCTCTGATTTATAGTGAAGACCAAGACTGTTCCCAAGAGATA	946
Qy	781	AGCAGCGCAGCTGAACAGCCCAAGACTTATACCATCTTCCAAAGGCGGCAAAAGAC	840
Db	947	AGCAGCGCAGCTGAACAGCCCAAGACTTATACCATCTTCCAAAGGCGGCAAAAGAC	1006
Qy	841	TGGGATAAATCGGAAGCTGAAGTCAAAAGAGGAGAGGAAAGAAACCTTGTATGTTGAT	900
Db	1007	TGGGATAAATCGGAAGCTGAAGTCAAAAGAGGAGAGGAAAGAAACCTTGTATGTTGAT	1066
Qy	901	GCTGCAATTTGAACAAATTTCTTCCGCTGATCTACAGGATGCTGATGAAGATATCGGAGG	960
Db	1067	GCTGCAATTTGAACAAATTTCTTCCGCTGATCTACAGGATGCTGATGAAGATATCGGAGG	1126
Qy	961	GCCATGATGAAGTCAATTCGTTGGAATCAAAATGGCACTGTTCTCTCAACCAATTTGAAAGAT	1020
Db	1127	GCCATGATGAAGTCAATTCGTTGGAATCAAAATGGCACTGTTCTCTCAACCAATTTGAAAGAT	1186

QY	1021	GTTCGAGCANAAGGTGTAAGAGGGAGCCCCCTTGATGTGAGCTCAAGAGTGGGAA	1080
24	1187	GTTCGATCATAATCGTTGGTAATGAGAGCCCTCTCGATGTGAGCTCAAGAGTGGGAA	1246

RESULT 7
US-10-425-115-18041
Sequence 18041, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 18041
LENGTH: 1519
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MFT4577_116456C.1
US-10-425-115-18041

Query Match	90.0%	Score 977.6;	DB 18;	Length 1519;
Best Local Similarity	94.1%	Pred. NO. 4.7e-281;		
Matches 1016;	Conservative	0;	Mismatches 64;	Indels 0;
Gaps	0			

QY	1	ATGCCGCGTTCGGATCTCGAGACGAAGGCCAAGGAGGCGCTTCGTGCGACGACGCTTCGAG	60
DB	167	ATGCCGCGTTCGGATCTCGAGACGAAGGAGGCGCTTCGTGCGAGCAGCTTCGAG	226
QY	61	CTGGCCACCGAGCTCTACAGCCAGGCGCATCGACGCGGGCGGCCACCGCGACCTCTAT	120
DB	227	CTGGCGCGCGAACTCTACACGAGGCGCATCGACGCGGGCGGCCACCTGCCCATCTCTAC	286
QY	121	GCCGACCGCGCCAGCGCGCACATCAAGCTTCGGCGCAACTACACTGAGGCTGTGGCGGATGCT	180
DB	287	GCCGACCGCGCCAGCGCGCATCAAGCTTCGGCGCAACTACACTGAGGCTGTGGCAGATGCT	346
QY	181	AACAAAGCAATTGAGCTTGATCCTATGATGCAATAAGCTTACTACCGGAAAGGTGCTGCA	240
DB	347	AACAAAGCAATTTGGTCTTGATCCTCAAAATGCAATAAGGCTACTACCGGAAAGGTGCTGCA	406
QY	241	TGCATTTAGCTTTGAGAATAACCAAACTGCAGGCGCTCTTGAGTTGGGTTCTTCTTAT	300
DB	407	TGCATTTAGCTTTGAGAATAACCAAACTGCAGGCGCTCTTGAGTTAGTTCTTCTTAT	466
QY	301	GCATCAGGCGAATTCAGGTTTGCTCTCTATTGAGGAATGTGATGAGCGCATTCGCTGAG	360
DB	467	GCACCGGCGAATTCAGGTTTACCCGCTATTGAGGAATGTGATGAGTGCATTTGCTGAG	526
QY	361	GAATCTAGCCAGGCACACAGTAAGAATGTTGAGGCTACTGTGCTGCTACTATTGAGGAC	420
DB	527	GAATCTAGCCAGGCACACAGTAAGAATGTCGAGGCTCCTGTAGCTGCTACTGTGTTGAGGAC	586
QY	421	AAGGAGGATTTCAAAATATGGAGAAATACACACCAAGTGTGATGAACCCCAAGCAAAACCA	480
DB	587	AAGGAGGATGTCGCAATATGGATATATACCCGCGAGTGGTAGNACCCCAAGCAAAACCT	646
QY	481	AAATACAGGCATGACTACTACAACAGTGCCACAGAAAGTGTA CTGCAATATTTGCTTAAG	540
DB	647	AAATATAGGCATGACTACTACAACAGTGCCACAGAAAGTGTCCTCAAAATATATGCTTAAG	706
QY	541	GGTGTTCTCTGCTGATAGTGTAGTCAATGATTTTGGTGAAACAGATGTTGAGTGATCCATT	600
DB	707	GGTGTTCTCTGCTGATAGTGTAGTCAATGATTTTGGTGATCAGATGTTGAGTGATCCATT	766
QY	601	GAAGTTCTCTGCTGAAGAACCATACCATTTTTCAGCCCCGTCGTGTTTCTCAAGATTTATCCCT	660

Db	767	GAAGTACCTGGTGAAGAACGGTACCAATTTTCAGCCCGCTGTGTTTCTAAGATTATCCCT	826
Qy	661	GAGAAATGCAAAATATCAAGTCTTTATCCACAAGGTTGAAATACGCCTTGCAAAAGCTGAG	720
Db	827	GAGAAATGCAAGTATCAAGTTTATCCACAAGGTCGAAATACGCCTTGCAAAAGCTGAG	886
Qy	721	CAGGTGACATGGGCAACCCCTGGATTATAGTGGGAAGCAAGACTGTTCCCAAGAGATA	780
Db	887	CAGGTGACATGGACAACCCCTGGATTATAGTGGGAAGCCAAAGGCTATTTCCCAAGAGATA	946
Qy	781	AGCAGCCAGCTGAAACAGGCCCCCAAGACCTTCATACCCATCTTCAAAAGCGCAAAAAGAC	840
Db	947	AGCAGCCAGCTGAAACAGGCCCCCAAGACCTTCATACCCATCTTCAAAAGTCAAAAAGGAC	1006
Qy	841	TGGGATAAATCTGGAAGCTGAAAGTCAAAAAGGAGGAGGAAGAAATCTGATGGTGAT	900
Db	1007	TGGGATAAATCTGGAAGCTGAAAGTCAAAAAGGAGGAGGAAGGAAGAAATCTGAAAGTGAT	1066
Qy	901	GCTGCATTGAACAAATCTTCCGTGACATCTACAAGGATGCTGATGAAGATATCGCGAGG	960
Db	1067	GCTGCATTGAACAAATCTTCCGTGATATCTACAAGGATGCTGATGAAGATATCGCGAGG	1126
Qy	961	GCCATGATGAAGTCAATTCGTGGAAATCAAAATGGCACTGTTCTCTCAACCAATTTGGAAGAT	1020
Db	1127	GCCATGACAAGTCATTCAGGGAATCTAATGGTACCGTTCTCTCAACCAATTTGGAAGAT	1186
Qy	1021	GTTGGAGCAAGAGGTAGAAGGGAGCCCCCTGATGATGGAGCTCAAGAAGTGGGAA	1080
Db	1187	GTTGGATCAAGAAGCGGTGGAAGCGAGCCCTCTGATGATGGAGCTCAAGAAGTGGGAA	1246

RESIST 8

RESULT 8
 US-10-425-114-24871
 ; Sequence 24871, Application US/10425114
 ; Publication No..US20040034889A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 24871
 ; LENGTH: 1649
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3689-210-C7_FLI
 ; US-10-425-114-24871

	Query Match	79.4%;	Score 862;	DB 17;	Length 1649;
	Best Local Similarity	83.5%;	Pred. No. 1.8e-246;		
	Matches 1086;	Conservative 0;	Mismatches 0;	Indels 214;	Gaps 1;
QY	1	ATGCCCGGTCGGATCTGGAGACCAAGCCAAAGGAGGCCCTTCGTCGACGACACTTCGAG	60		
DB	91	ATGCCCGGTCGGATCTGGAGACCAAGCCAAAGGAGGCCCTTCGTCGACGACACTTCGAG	150		
QY	61	CTGGCCACCGAGCTCTACGACGAGGCCATCGACGCCGGGCCGCCACCGCGGACCTCTAT	120		
DB	151	CTGGCCACCGAGCTCTACGACGAGGCCATCGACGCCGGGCCGCCACCGCGGACCTCTAT	210		
QY	121	GCCGACCGGCCCGCCAGGCGCACATCAAGCTCGGCGCACTACACTGAGGCGTGTGGCGGATGCT	180		
DB	211	GCCGACCGGCCCGCCAGGCGCACATCAAGCTCGGCGCACTACACTGAGGCGTGTGGCGGATGCT	270		

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1861	100.0	388	15	US-10-435-114-61162	Sequence 6
2	1861	100.0	390	15	US-10-425-114-61204	Sequence 6
3	1771.5	95.2	395	16	US-10-767-701-45515	Sequence 4
4	1740	93.5	393	15	US-10-435-114-61212	Sequence 6
5	1740	93.5	416	15	US-10-435-114-65836	Sequence 6
6	1578	84.8	376	16	US-10-437-963-139712	Sequence 1
7	1263	67.9	256	15	US-10-425-114-61200	Sequence 6
8	1176.5	63.2	357	15	US-10-424-539-224769	Sequence 2
9	1146.5	61.6	359	15	US-10-424-559-208541	Sequence 2
10	925.5	49.7	357	15	US-10-424-559-241114	Sequence 2
11	729	39.2	160	15	US-10-424-559-261373	Sequence 2
12	615	33.0	344	15	US-10-264-049-3093	Sequence 3
13	603.5	32.4	223	16	US-10-437-963-146392	Sequence 1

88 NKAIEIDPMMHKAY

1	MAASDLESKAKEAFVDDDDFLATATELYSQAIDAGPATADLYADRAQAHIKLGNTEAVADA	60
28	MAASDLESKAKEAFVDDDDFLATATELYSQAIDAGPATADLYADRAQAHIKLGNTEAVADA	87
61	NKAIELDDPMHKAAYYRKGAACIKLEESYQTKAALELGSSYASGDSRFARLLKCEDSERIAE	120
88	NKAIELDDPMHKAAYYRKGAACIKLEEVOTKAALELGSSYASGDSRFARLLKCEDSERIAE	147

Qy 121 ESSQAPVKNVEATVAATIBDKEDFTNMENTPPVIEPPSPKPKYRHDYNSATEVLTIPAK 180
 |||||
 Db 148 ESSQAPVKNVEATVAATIBDKEDFTNMENTPPVIEPPSPKPKYRHDYNSATEVLTIPAK 207
 |||||
 Qy 181 GVPADSVVIDFGEOMLSVSIIEVPGEPYHFQRLFSKIIPKCKYQVLTSTKVEIRLAKAE 240
 |||||
 Db 208 GVPADSVVIDFGEOMLSVSIIEVPGEPYHFQRLFSKIIPKCKYQVLTSTKVEIRLAKAE 267
 |||||
 Qy 241 QVTTTLDYSGRPKTVPOKISTPAETAPRPSYPSSKAKKDWKLEAEVKKEEKLGDG 300
 |||||
 Db 268 QVTTTLDYSGRPKTVPOKISTPAETAPRPSYPSSKAKKDWKLEAEVKKEEKLGDG 327
 |||||
 Qy 301 AALNKKFRDIYKDADEDMRRAMKSFVESNGTVLSTNNKDVGAKKVEGSPDPGMLKKWE 360
 |||||
 Db 328 AALNKKFRDIYKDADEDMRRAMKSFVESNGTVLSTNNKDVGAKKVEGSPDPGMLKKWE 387
 |||||
 Qy 361 Y 361
 |||||
 Db 388 Y 388

RESULT 2

US-10-425-114-61204
 ; Sequence 61204, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 61204
 ; LENGTH: 390
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3732-024-C2_FLI.pep
 US-10-425-114-61204

Query Match 100.0%; Score 1861; DB 15; Length 390;
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;
 Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MAASDLESKAKEAFVDDDFELATLAYSQAIDAGPATADLYADRAQAHIKLGNYTEAVADA 60
 |||||
 Db 30 MAASDLESKAKEAFVDDDFELATLAYSQAIDAGPATADLYADRAQAHIKLGNYTEAVADA 89
 |||||
 Qy 61 NKAILEDPMHKAAYRKGAACIKLEEYQTAKAALGSSYASGDSRPFARLLKECDERIAE 120
 |||||
 Db 90 NKAILEDPMHKAAYRKGAACIKLEEYQTAKAALGSSYASGDSRPFARLLKECDERIAE 149
 |||||
 Qy 121 ESSQAPVKNVEATVAATIBDKEDFTNMENTPPVIEPPSPKPKYRHDYNSATEVLTIPAK 180
 |||||
 Db 150 ESSQAPVKNVEATVAATIBDKEDFTNMENTPPVIEPPSPKPKYRHDYNSATEVLTIPAK 209
 |||||
 Qy 181 GVPADSVVIDFGEOMLSVSIIEVPGEPYHFQRLFSKIIPKCKYQVLTSTKVEIRLAKAE 240
 |||||
 Db 210 GVPADSVVIDFGEOMLSVSIIEVPGEPYHFQRLFSKIIPKCKYQVLTSTKVEIRLAKAE 269
 |||||
 Qy 241 QVTTTLDYSGRPKTVPOKISTPAETAPRPSYPSSKAKKDWKLEAEVKKEEKLGDG 300
 |||||
 Db 270 QVTTTLDYSGRPKTVPOKISTPAETAPRPSYPSSKAKKDWKLEAEVKKEEKLGDG 329
 |||||
 Qy 301 AALNKKFRDIYKDADEDMRRAMKSFVESNGTVLSTNNKDVGAKKVEGSPDPGMLKKWE 360
 |||||

Db 330 AALNKKFRDIYKDADEDMRRAMKSFVESNGTVLSTNNKDVGAKKVEGSPDPGMLKKWE 389
 Qy 361 Y 361
 Db 390 Y 390
 RESULT 3
 US-10-767-701-45515
 ; Sequence 45515, Application US/10767701
 ; Publication No. US20040172884A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5353)B
 ; CURRENT APPLICATION NUMBER: US/10/767,701
 ; CURRENT FILING DATE: 2004-01-29
 ; NUMBER OF SEQ ID NOS: 63128
 ; SEQ ID NO 45515
 ; LENGTH: 395
 ; TYPE: PRT
 ; ORGANISM: Sorghum bicolor
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(395)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C2718_1.pep
 US-10-767-701-45515

Query Match 95.2%; Score 1771.5; DB 16; Length 395;
 Best Local Similarity 94.2%; Pred. No. 3.2e-130;
 Matches 343; Conservative 7; Mismatches 11; Indels 3; Gaps 1;
 Qy 1 MAASDLESKAKEAFVDDDFELATLAYSQAIDAGPATADLYADRAQAHIKLGNYTEAVADA 60
 |||||
 Db 32 MAASDLESKAKEAFVDDDFELATLAYSQAIDAGPATADLYADRAQAHIKLGNYTEAVADA 91
 |||||
 Qy 61 NKAILEDPMHKAAYRKGAACIKLEEYQTAKAALGSSYASGDSRPFARLLKECDERIAE 120
 |||||
 Db 92 NKAILEDPMHKAAYRKGAACIKLEEYQTAKAALGSSYASGDSRPFARLLKECDERIAE 151
 |||||
 Qy 121 ESSQAPVKNVEATVAATIBDKEDFTNMENTPPVIEPPSPKPKYRHDYNSATEVLTIPAK 177
 |||||
 Db 152 ESSQAPVKNVEATVAATIBDKEDFTNMENTPPVIEPPSPKPKYRHDYNSATEVLTIPAK 211
 |||||
 Qy 178 FAKGVPADSVVIDFGEOMLSVSIIEVPGEPYHFQRLFSKIIPKCKYQVLTSTKVEIRLA 237
 |||||
 Db 212 FAKGVPADSVVIDFGEOMLSVSIIEVPGEPYHFQRLFSKIIPKCKYQVLTSTKVEIRLA 271
 |||||
 Qy 238 KAEQVTTTLDYSGRPKTVPOKISTPAETAPRPSYPSSKAKKDWKLEAEVKKEEKL 297
 |||||
 Db 272 KAEQVTTTLDYSGRPKTVPOKISTPAETAPRPSYPSSKAKKDWKLEAEVKKEEKL 331
 |||||
 Qy 298 DGDAALNKKFRDIYKDADEDMRRAMKSFVESNGTVLSTNNKDVGAKKVEGSPDPGMLK 357
 |||||
 Db 332 DGDAALNKKFRDIYKDADEDMRRAMKSFVESNGTVLSTNNKDVGAKKVEGSPDPGMLK 391
 |||||
 Qy 358 KWEY 361
 |||||
 Db 392 KWEY 395

RESULT 4

US-10-425-114-61212
 ; Sequence 61212, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua

/ APPLICANT: Kovalic, David K.
 / APPLICANT: Screen, Steven E
 / APPLICANT: Tabaska, Jack E
 / APPLICANT: Cao, Yongwei
 / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(53313)B
 / CURRENT APPLICATION NUMBER: US/10/425,114
 / CURRENT FILING DATE: 2003-04-28
 / NUMBER OF SEQ ID NOS: 73128
 / SEQ ID NO 61212
 / LENGTH: 393
 / TYPE: PRT
 / ORGANISM: Zea mays
 / FEATURE:
 / OTHER INFORMATION: Clone ID: LIB3960-013-B4_FLI.pep
 US-10-425-114-61212

Query Match 93.5%; Score 1740; DB 15; Length 393;
 Best Local Similarity 93.1%; Pred. No. 9.3e-128;
 Matches 335; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MAASDLESKAKEAFVDDDDFELATLYSOAIDAGPATADLYADRAQAHIKLGNYTEAVADA 60
 DB 33 MAASDLESKAKEAFVDDDDFELAAELYTQADAGPATADLYADRAQAHIKLGNYTEAVADA 92
 QY 61 NKAIELDPMMHKAYYRKGAAACIKLEEQYQAKAAELGSSYASGDSRFRLLKCEDEIAE 120
 DB 93 NKAIGLDPMMHKAYYRKGAAACIKLEEQYQAKAAELGSSYASGDSRFRLLKCEDEIAE 152
 QY 121 ESSQAPKVNVEATVAATIEDKEDFTNMNTPPVIEPPSKPKYRHDYNSATEVVLTIYAK 180
 DB 153 ESSQAPKVNVEATVAATIEDKEDVANNDNTPPVIEPPSKPKYRHDYNSATEVVLTIYAK 212
 QY 181 GVPADSVVIDFGQMLSVSIEVPGEPYHPQPLFSKIIPEKCKYQVLSKVEIRLAKAE 240
 DB 213 GVPADSVVIDFGQMLSVSIEVPGEPYHPQPLFSKIIPEKCKYQVLSKVEIRLAKAE 272
 QY 241 QVTWTTLDYSGRPKTPQKISTPAETAPRPSYSSKAKDMDKLEAEVKKKEEKLGD 300
 DB 273 QVTWTTLDYSGRPKTPQKISTPAETAPRPSYSSKAKDMDKLEAEVKKKEEKLGD 332
 QY 301 AALNKFRIYKDADMRAMKSFVESNGTVLSTNWKDVGAKYVGGSPDGMELKKWE 360
 DB 333 AALNKFRIYKDADMRAMKSFVESNGTVLSTNWKDVGAKYVGGSPDGMELKKWE 392

RESULT 5
 US-10-425-114-65836
 / Sequence 65836, Application US/10425114
 / Publication No. US20040034888A1
 / GENERAL INFORMATION:
 / APPLICANT: Liu, Jingdong
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Kovalic, David K.
 / APPLICANT: Screen, Steven E
 / APPLICANT: Tabaska, Jack E
 / APPLICANT: Cao, Yongwei
 / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(53313)B
 / CURRENT APPLICATION NUMBER: US/10/425,114
 / CURRENT FILING DATE: 2003-04-28
 / NUMBER OF SEQ ID NOS: 73128
 / SEQ ID NO 65836
 / LENGTH: 416
 / TYPE: PRT
 / ORGANISM: Zea mays
 / FEATURE:
 / OTHER INFORMATION: Clone ID: LIB3591-005-25_FLI.pep
 US-10-425-114-65836

Query Match 93.5%; Score 1740; DB 15; Length 416;

Best Local Similarity 93.1%; Pred. No. 1e-127;
 Matches 335; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MAASDLESKAKEAFVDDDDFELATLYSOAIDAGPATADLYADRAQAHIKLGNYTEAVADA 60
 DB 56 MAASDLESKAKEAFVDDDDFELAAELYTQADAGPATADLYADRAQAHIKLGNYTEAVADA 115
 QY 61 NKAIELDPMMHKAYYRKGAAACIKLEEQYQAKAAELGSSYASGDSRFRLLKCEDEIAE 120
 DB 116 NKAIGLDPMMHKAYYRKGAAACIKLEEQYQAKAAELGSSYASGDSRFRLLKCEDEIAE 175
 QY 121 ESSQAPKVNVEATVAATIEDKEDFTNMNTPPVIEPPSKPKYRHDYNSATEVVLTIYAK 180
 DB 176 ESSQAPKVNVEATVAATIEDKEDVANNDNTPPVIEPPSKPKYRHDYNSATEVVLTIYAK 235
 QY 181 GVPADSVVIDFGQMLSVSIEVPGEPYHPQPLFSKIIPEKCKYQVLSKVEIRLAKAE 240
 DB 236 GVPADSVVIDFGQMLSVSIEVPGEPYHPQPLFSKIIPEKCKYQVLSKVEIRLAKAE 295
 QY 241 QVTWTTLDYSGRPKTPQKISTPAETAPRPSYSSKAKDMDKLEAEVKKKEEKLGD 300
 DB 296 QVTWTTLDYSGRPKTPQKISTPAETAPRPSYSSKAKDMDKLEAEVKKKEEKLGD 355
 QY 301 AALNKFRIYKDADMRAMKSFVESNGTVLSTNWKDVGAKYVGGSPDGMELKKWE 360
 DB 356 AALNKFRIYKDADMRAMKSFVESNGTVLSTNWKDVGAKYVGGSPDGMELKKWE 415

RESULT 6
 US-10-437-963-139712
 / Sequence 139712, Application US/10437963
 / Publication No. US20040123343A1
 / GENERAL INFORMATION:
 / APPLICANT: La Rosa, Thomas J.
 / APPLICANT: Kovalic, David K.
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Cao, Yongwei
 / APPLICANT: Wu, Wei
 / APPLICANT: Boukharov, Andrey A.
 / APPLICANT: Barbazuk, Brad
 / APPLICANT: Li, Ping
 / TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(53221)B
 / CURRENT APPLICATION NUMBER: US/10/437,963
 / CURRENT FILING DATE: 2003-05-14
 / NUMBER OF SEQ ID NOS: 204966
 / SEQ ID NO 139712
 / LENGTH: 376
 / TYPE: PRT
 / ORGANISM: Oryza sativa
 / FEATURE:
 / OTHER INFORMATION: Clone ID: PAT_MRT4530_40977C.1.pap
 US-10-437-963-139712

Query Match 84.8%; Score 1578; DB 16; Length 376;
 Best Local Similarity 82.1%; Pred. No. 4.2e-115;
 Matches 307; Conservative 27; Mismatches 24; Indels 16; Gaps 3;
 QY 2 AASDLESKAKEAFVDDDDFELATLYSOAIDAGPATADLYADRAQAHIKLGNYTEAVADA 61
 DB 5 AASDLESKAKEAFVDDDDFELAAELYTQADAGPATADLYADRAQAHIKLGNYTEAVADA 64
 QY 62 KAIELDPMMHKAYYRKGAAACIKLEEQYQAKAAELGSSYASGDSRFRLLKCEDEIAE 121
 DB 65 KAIELDPMMHKAYYRKGAAACIKLEEQYQAKAAELGSSYASGDSRFRLLKCEDEIAE 124
 QY 122 SSQAPKVNVEATVAATIEDKEDFTNMNTPPVIEPPSKPKYRHDYNSATEVVLTIYAK 176
 DB 125 LSEVPVTKAEDGAAAPSVASFVEEKDDAANNNDNTPPMVVE--VKPKYRHDYNSATEVVLTIYAK 182
 QY 177 IFAGKVPADSVVIDFGQMLSVSIEVPGEPYHPQPLFSKIIPEKCKYQVLSKVEIRL 236

Db 183 IPAGVPAENVVDFGEQMLSVSIEVPGEEYHFQPRLFKSIIPKSRKYQVLSTKVEIRL 242
 QY 237 AKAEQVTTWTLTLDYSGRPKTVPOKISTP-----AETAPRPSYPSSKAKKDWKLEAE 287
 Db 243 AKAEQITWTLTLDYDKKPAVPOKIPVPLVLLIALLSAESAQPSYPSSKSKDWKLEAE 302
 QY 288 VKKEEKEKLDGDAALNKFRRDIYKDADEDMRAMMKSFVESNGTVLSTNNKDWGAKKVE 347
 Db 303 VKKEEKEKLDGDAALNKFRRDIYSDADEDMRAMMKSFVESNGTVLSTNNKDWGSKKVE 362
 QY 348 GSPDPGMELKKWEY 361
 Db 363 GSPDPGMELKKWEY 376

RESULT 7

US-10-425-114-61200
 ; Sequence 61200, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Li, Jingdong
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; NUMBER OF SEQ ID NOS: 2003-04-28
 ; CURRENT FILING DATE: 2003-04-28
 ; SEQ ID NO 61200
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3689-210-C7_FLI.pep
 US-10-425-114-61200

Query Match 67.9%; Score 1263; DB 15; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.1e-90;
 Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 120 BESSQAPKVNVEATVAATIEDKEDFTNMTPPPVIEPPSPKRYRHDYNSATEVLTIFA 179
 Db 15 BESSQAPKVNVEATVAATIEDKEDFTNMTPPPVIEPPSPKRYRHDYNSATEVLTIFA 74
 QY 180 KGVPADSVVIDFGEQMLSVSIEVPGEEYHFQPRLFKSIIPKSKYQVLSTKVEIRLAKA 239
 Db 75 KGVPADSVVIDFGEQMLSVSIEVPGEEYHFQPRLFKSIIPKSKYQVLSTKVEIRLAKA 134
 QY 240 EQVTTWTLTLDYSGRPKTVPOKISTPABTAPRPSYPSSKAKKDWKLEAEVKKKEEKLGD 299
 Db 135 EQVTTWTLTLDYSGRPKTVPOKISTPABTAPRPSYPSSKAKKDWKLEAEVKKKEEKLGD 194
 QY 300 DAALNKFRRDIYKDADEDMRAMMKSFVESNGTVLSTNNKDWGAKKVEGSPDGMELKKW 359
 Db 195 DAALNKFRRDIYKDADEDMRAMMKSFVESNGTVLSTNNKDWGAKKVEGSPDGMELKKW 254
 QY 360 EY 361
 Db 255 EY 256

RESULT 8

US-10-424-599-224769
 ; Sequence 224769, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J
 ; APPLICANT: Kovalic, David K
 ; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; NUMBER OF SEQ ID NOS: 2003-04-28
 ; SEQ ID NO 224769
 ; LENGTH: 357
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(357)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_44998C.1.pep
 US-10-424-599-224769

Query Match 63.2%; Score 1176.5; DB 15; Length 357;
 Best Local Similarity 64.5%; Pred. No. 1e-83;
 Matches 234; Conservative 48; Mismatches 68; Indels 13; Gaps 6;
 QY 3 ASDLESKAKGAFVDDDFELATYLSQADIDAGPATADLYADRAQAHIKLGNYTEAVADANK 62
 Db 2 ASDLELKAKGAFEDDDNYDLAYDLLTQAIGLSPNNADLYADRAQVNIKVNLLTEAVSDANK 61
 QY 63 AIELDPMMHRYKRGACIKLEEVOTAKALELSSVAGSDSRFARLLKCEDERIAEES 122
 Db 62 AIELNPSHSHKAYLRKGTACIKLEBYQTAKALENGSLAPGDSKFTDLKOCDELIABES 121
 QY 123 SQAPVQKVNVEATVAATIEDKEDFTNMTPPPVIEPPS-----KPKYRHDYNSATEVLTIF 178
 Db 122 GVPIQESITQGAATRAVE-----AENDLP--EPTVTWVKPYRHEFYQKPDENVITIF 175
 QY 179 AKGVPADSVVIDFGEQMLSVSIEVPGEEYHFQPRLFKSIIPKSKYQVLSTKVEIRLAK 238
 Db 176 AKGIFRDSITVDFGEQILSVTINIPCKDAYVFOQPRLFKSIIPSKRYEVLSTKIEICLAK 235
 QY 239 AEQVTTWTLTLDYSGRPKTVPOKIST-PAETAPRPSYPSSKAKK-DWDKLEAEVKKKEEKEK 296
 Db 236 ADHIQWTSLEFN-KGSTVAQRFSVLPVARGEKPTIPSSKPKKXDWKLEAEVKKKEEKEK 294
 QY 297 LDGDAALNKFRRDIYKDADEDMRAMMKSFVESNGTVLSTNNKDWGAKKVEGSPDGMEL 356
 Db 295 LDGDAALNKFRRDIYQDADSDTRAMSKSFVESNGTVLSTNNKVEGSMKVKQESPPDGMEL 354
 QY 357 KKW 359
 Db 355 KKW 357

RESULT 9

US-10-424-599-208541
 ; Sequence 208541, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J
 ; APPLICANT: Kovalic, David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; NUMBER OF SEQ ID NOS: 2003-04-28
 ; SEQ ID NO 208541
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_30341C.1.pep

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 23, 2005, 00:00:36 ; Search time 3903.36 Seconds
(without alignments)
10590.311 Million cell updates/sec

Title: US-10-609-078-9
Perfect score: 1086
Sequence: 1 atggcgctgcgatctgga.....tcaagaagtggaataactaa 1086

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1068.4	98.4	1646	3 AY103953	AY103953 Zea mays
2	698.2	64.3	1131	9 CL959360	CL959360 OeIFCC002
3	652.4	60.1	668	2 AW076274	AW076274 614063D11
4	650.2	59.9	752	6 CD443320	CD443320 EL01N0424
5	647	59.6	756	6 CA184150	CA184150 SCRFST314
6	643.4	59.2	659	2 AW090936	AW090936 614068G07
7	643.4	59.2	772	6 CA258233	CA258233 SCCRT300
8	641	59.0	759	6 CA245820	CA245820 SCEZF508
9	631	58.1	666	6 CA215140	CA215140 SC9BAD112
10	608.2	56.0	678	6 CA177070	CA177070 SCWCST105
11	607	55.9	665	6 CA153735	CA153735 SCVPR2203
12	596.4	54.9	622	6 CA229980	CA229980 SCUFPL3C0
13	583.4	53.7	586	2 AW042392	AW042392 614028B03
14	583.4	53.7	609	6 CA229238	CA229238 SCAGFL302
15	572	52.7	702	6 CA262995	CA262995 SCPRLB202
16	566	52.1	718	6 CA106435	CA106435 SCQHR101
17	565.2	52.0	594	6 CA098274	CA098274 SCMCC605
18	562	51.7	574	4 B1644145	B1644145 949022C08
19	557.2	51.3	630	6 CA486265	CA486265 WHE4329 D
20	555.6	51.2	579	2 AW066518	AW066518 660015G08
21	552.8	50.9	680	6 CA128103	CA128103 SCAGLR203
22	550	50.6	550	4 B1679413	B1679413 949001E02
23	550	50.6	914	6 CA084222	CA084222 SCEQAW203
24	545	50.2	588	5 BU499669	BU499669 946178B11

25	541	49.8	601	6 CA176126	CA176126 SCJLST102
26	535.8	49.3	553	5 BU098322	BU098322 946134B07
27	529.4	48.7	612	6 CA234143	CA234143 SCCCL6C0
28	523	48.2	615	6 CA283412	CA283412 SCSBSD105
29	522.6	48.1	730	2 BE362001	BE362001 DGI 83 H0
30	520.8	48.0	725	6 CA094787	CA094787 SCCCL401
31	520.8	47.9	578	6 CD996630	CD996630 QSC6A07.X
32	519.6	47.8	708	6 CA240596	CA240596 SCSBFL406
33	514.8	47.4	1089	7 CK208966	CK208966 FGAS02069
34	512.2	47.2	693	6 CA104899	CA104899 SCJFHR1C0
35	511.6	47.1	606	6 CA083869	CA083869 SCEPAM205
36	508.4	46.8	625	6 CA266503	CA266503 SCAGLB204
37	507.4	46.7	518	2 AW057009	AW057009 66007D01
38	507.4	46.7	862	6 CB655564	CB655564 OSJNEC09B
39	507.2	46.7	652	6 CA102017	CA102017 SCAGHR101
40	505.2	46.5	798	6 CA176210	CA176210 SCJLST102
41	500.6	46.1	610	6 CA184034	CA184034 SCQSSST11
42	499.4	46.0	643	6 CA251380	CA251380 SCQSPFL112
43	498.8	45.9	778	6 CA227695	CA227695 SCJLFL301
44	498.4	45.9	607	6 CA120629	CA120629 SCCCLR108
45	487.4	44.9	792	6 CB657723	CB657723 OSJNEC13E

ALIGNMENTS

RESULT 1
LOCUS AY103953 1646 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PC0098564 mRNA sequence.
ACCESSION AY103953
VERSION AY103953.1 GI:21207031
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 1646)
AUTHORS Hainey C.F., Dolan M., Miao G.H., Vogel J.M., Whittitt M.S., Arthur L.W., Hanafey M., Morgante M. and Tingey S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1646)
AUTHORS Coe E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES
Location/Qualifiers
1..1646
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:635643"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 98.4%; Score 1068.4; DB 3; Length 1646;

Best Local Similarity 99.0%; Pred. No. 2.le-288; Matches 1075; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGCGCCGCTCGATCTGAGACGAAGGCCAAGGAGGCTTGTTCGACGACACTTCGAG 60

DB 201 ATGCGCCGCTCGATCTGAGACGAAGGCCAAGGAGGCTTGTTCGACGACACTTCGAG 260

QY 61 CTGGCCACCAGAGCTTTACAGCAGGCGCATCGACGCGGCGCCGCCACCGCCGACCTCTAT 120

DB 261 CTGGCCACCAGAGCTTTACAGCAGGCGCATCGACGCGGCGCCGCCACCGCCGACCTCTAT 320

QY 121 GCGACGCGCGCCGCGCACATCAAGCTCGGCACCTACATGAGGCTGTGGCGGATGCT 180

DB 321 GCGACGCGCGCCGCGCACATCAAGCTCGGCACCTACATGAGGCTGTGGCGGATGCT 380

QY 181 AACAAAGCAATTGAGCTTGATCTATGATGATAAAGCTTACTACCGGAAGAGTCTGCA 240

DB 381 AACAAAGCAATTGAGCTTGATCTATGATGATAAAGCTTACTACCGGAAGAGTCTGCA 440

QY 241 TGCAATTAAGCTTGAAGAATACCAAATCGCAAGGCTGCTTTGAGTGGGTTCTTCTTAT 300

DB 441 TGCAATTAAGCTTGAAGAATACCAAATCGCAAGGCTGCTTTGAGTGGGTTCTTCTTAT 500

QY 301 GCATCAGCGATTCAAGGTTGCTGCTCTATTGAGGAAATGTGATGAGGCAATCGCTGAG 360

DB 501 GCATCAGCGATTCAAGGTTGCTGCTCTATTGAGGAAATGTGATGAGGCAATCGCTGAG 560

QY 361 GAATCTAGCCAGGCAACCAAGTAAGTAAGTGTGAGGCTACTGTGGCTGTACTATTGAGGAC 420

DB 561 GAATCTAGCCAGGCAACCAAGTAAGTAAGTGTGAGGCTACTGTGGCTGTACTATTGAGGAC 620

QY 421 AAGGAGGATTTCAAAATATGAGGAATACACAACAGGTGATAGAACCCCAAGCAACCA 480

DB 621 AAGGAGGATTTCAAAATATGAGGAATACACAACAGGTGATAGAACCCCAAGCAACCA 680

QY 481 AAATACAGCATGACTACTACAGAGTCCACAGAGTGTACTGACAAATTTGCTTAAG 540

DB 681 AAATACAGCATGACTACTACAGAGTCCACAGAGTGTACTGACAAATTTGCTTAAG 740

QY 541 GGTTGTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

DB 741 GGTTGTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800

QY 601 GAAGTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

DB 801 GAAGTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 860

QY 661 GAGAAATGCAATATCAAGTCTTATCCACAGGTTGAAATACGCTTGCMAAAGCTGAG 720

DB 861 GAGAAATGCAATATCAAGTCTTATCCACAGGTTGAAATACGCTTGCMAAAGCTGAG 920

QY 721 CAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780

DB 921 CAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 980

QY 781 AGCAGCGAGCTGAAAAGCCCCAAGACCTTCAATCCCATCTTCAAAAGGCGAAAAAGAC 840

DB 981 AGCAGCGAGCTGAAAAGCCCCAAGACCTTCAATCCCATCTTCAAAAGGCGAAAAAGAC 1040

QY 841 TGGGATAAATCTGGAAGCTGAAGTCAAAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 900

DB 1041 TGGGATAAATCTGGAAGCTGAAGTCAAAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1100

QY 901 GCTGCATTGAACAAATTTCTTCCGTGATCTTACAGGATGCTGATGAAGATATGCGGAGG 960

DB 1101 GCTGCATTGAACAAATTTCTTCCGTGATCTTACAGGATGCTGATGAAGATATGCGGAGG 1160

QY 961 GCCATGATGAAGTCAATTCGTGGAATCAAAATGGCACTGTTCTTCAACCAATTGGAAGAT 1020

DB 1161 GCCATGATGAAGTCAATTCGTGGAATCAAAATGGCACTGTTCTTCAACCAATTGGAAGAT 1220

QY 1021 GTTGGAGCAAGAGGTAGAGGAGGCCCCCTGATGGTATGAGCTCAAGAGTGGGAA 1080

Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614063 row: D column: 11.
Location/Qualifiers
1..568
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W23"
/db_xref="taxon:4577"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLOLR"
/clone_lib="614 - root cDNA library from Walbot Lab"
/note="Organ: root; Vector: pBluescriptII SK+; Site 1:
ECOR1; Site 2: XhoI; 3-4 days old root tissue from Walbot
Lab (LM)"

7 CCATCTTCAAAGCGAAAAAGACTGGGATAAACTGGAAGCTGAAGTCAAAAAGGAGGAG 876
 4 CCATCTTCAAAGCGAAAAAGACTGGGATAAACTGGAAGCTGAAGTCAAAAAGGAGGAG 493
 7 AAGGAAGAAAACTTGATGTGATGCTGCATTGAACAAATCTTCCGTGACTCTACAAG 936
 4 AAGGAAGAAAACTTGATGTGATGCTGCATTGAACAAATCTTCCGTGACTCTACAAG 553
 7 GATCTGATGAAGATATCGCGAGGCGCCATGATGAAGTCAATCGTGGAAATCAAAATGGCACT 996
 4 GATCTGATGAAGATATCGCGAGGCGCCATGATGAAGTCAATCGTGGAAATCAAAATGGCACT 613
 7 GTTCTCTCAACCAATTGGAAAGATGTTGGAGCAAAAGAGGTAGAAGGGAGCCCC 1050
 4 GTTCTCTCAACCAATTGGAAAGATGTTGGAGCAAAAGAGGTAGAAGGGAGCCCC 667

CD443320 752 bp mRNA linear EST 03-JUN-2003

DEFINITION ELO1N0424G10.b Endosporm_4 Zea mays cDNA, mRNA sequence.

ACCESSION CD443320

VERSION CD443320.1 GI:31358963

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 752)

Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,

Larkin, B., Becraft, P. and Messing, J.

Characterization of the maize endosporm transcriptome and its

comparison to the rice genome

Genome Res. 14 (10), 1932-1937 (2004)

Contact: Lai, Jinheng

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Tel: 732-445-3801

Fax: 732-445-5735

Email: jlai@wakeman.rutgers.edu

Seq primer: T3.

Location/Qualifiers

1..752

/organism="Zea mays"

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/note="Vector: paluescript SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

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Best Local Similarity 99.5%; Pred. No. 4.9e-171;
Matches 652; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGCGCGGCTCGGATCTGGAGCAAGGCCAAGGAGGCTTCGTCGACGAGCTTCGAG 60

Db 98 ATGCGCGGCTCGGATCTGGAGCAAGGCCAAGGAGGCTTCGTCGACGAGCTTCGAG 157

Qy 61 CTGCGCCACCGAGCTCTACAGCCAGCCATCGACCGCGGCGCCGACCGCGAGCTCTAT 120

Db 158 CTGCGCCACCGAGCTCTACAGCCAGCCATCGACCGCGGCGCCGACCGCGAGCTCTAT 217

Qy 121 GCCGACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 180

Db 218 GCCGACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 277

Qy 181 AACAAAGCAATGAGCTTGATCTTATGATGATGATGATGATGATGATGATGATGATGAT 240

Db 278 AACAAAGCAATGAGCTTGATCTTATGATGATGATGATGATGATGATGATGATGATGAT 337

Qy 241 TGCATTAGCTTGAAGTAATACCAATGCAAGGCTGCTTTGAGTTGGGTTCTTCTTAT 300

Db 338 TGCATTAGCTTGAAGTAATACCAATGCAAGGCTGCTTTGAGTTGGGTTCTTCTTAT 397

Qy 301 GCATCAGCGGATTCAGGTTTGTCTCTATTAAGGATGATGATGATGATGATGATGATGATGAT 360

Db 398 GCATCAGCGGATTCAGGTTTGTCTCTATTAAGGATGATGATGATGATGATGATGATGATGAT 457

Qy 361 GAATCTAGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420

Db 458 GAATCTAGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 517

Qy 421 AAGGAGGATTTTCAAAATATGAGGAATACACCAAGTGTATGAGTATGAGTATGAGTATGAG 480

Db 518 AAGGAGGATTTTCAAAATATGAGGAATACACCAAGTGTATGAGTATGAGTATGAGTATGAG 577

Qy 481 AATATCAGGCGATGACTACTACACAGTGCACAGAGTGTACTGACATATTTTGCTAAG 540

Db 578 AATATCAGGCGATGACTACTACTACAGTGCACAGAGTGTACTGACATATTTTGCTAAG 637

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Db 638 GGTGTTCTCTCTGATAGTGTAGTCAATGATTTTGGTGAACAGATGTTGAGTGTATCCATT 697

Qy 601 GAAGTTCTCTGTTGAAGAACCATACCATTTTCAGCCCGCTCTGTTTCTAGATTA 655

Db 698 GAAGTTCTCTGTTGAAGAACCATACCATTTTCAGCCCGCTCTGTTTCTAGATTA 752

RESULT 5

CA184150

LOCUS

DEFINITION

CA184150

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Saccharum officinarum

Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum

complex.

REFERENCE

1 (bases 1 to 756)

Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parada@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

http://www.bcccenter.fcav.unesp.br

Plate: 142 row: H column: 05

Seq primer: T7 promoter Primer.

Location/Qualifiers

1..756

/organism="Saccharum officinarum"

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/db_xref="taxon:4547"

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/notes="Organ: Fourth apical stalk internodes of adult

plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An

unidirectional cDNA library generated from [Fourth apical

stalk internodes of adult plants]. cDNA was prepared from

polyA+ mRNA using SuperScript Plasmid System Kit

(Invitrogen). The double-strand cDNAs were fractionated

in a sepharose CL-2B 40cm-columns and fragments sizing

between 0.8 and 1.5 Kb were directionally cloned into the

vector. Details of each source of RNA and library

construction can be obtained at

http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match

Best Local Similarity

Matches

721; Conservative

0; Mismatches

32; Indels

6; Gaps

5;

Qy 4 GCGCGCTCGGATCTGAGAGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 63

Db 3 GCGCGCTCGGATCTGAGAGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 62

Qy 64 GCCACCGGAGCTCTACAGCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 123

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Lab (LM)"

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ORIGIN

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Best Local Similarity 99.8%; Pred. No. 3.8e-169;
Matches 644; Conservative 0; Mismatches 1; Indels 0; Gaps 0
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600	TGAAGTCTCTGGTGAAGAACATACCAATTTTCAGCCCGTCTGTTTCTTAAGATTATCCC	659
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Db		

DEC 11 7

RESULTS 7	CA258233	772 bp	linear	EST 26-SEP-2003
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DEFINITION	SCCCT3004D05.9	Rt3	Saccharum officinarum	cdna clone SCCRT3004D05
	5', mRNA sequence.			
ACCESSION	CA258233			
VERSION	CA258233.1			
KEYWORDS	EST.			
SOURCE	Saccharum officinarum			
ORGANISM	Saccharum officinarum			

FEATURES

RESULT 6	AW090936	659 bp	mRNA	linear	EST 18-OCT-1999
LOCUS	AW090936				
DEFINITION	G14068G07.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA, mRNA sequence.				
ACCESSION	AW090936				
VERSION	AW090936.1	GI:6056546			
KEYWORDS	EST.				
SOURCE	Zea mays				
ORGANISM	Zea mays *				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD				
	clade; Panicoideae; Andropogoneae; Zea.				
REFERENCE	1 (bases 1 to 659)				

AUTHORS WAIBOT, V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

University
 1000

JOURNAL
COMMENT
Unpublished (1999)
Contact: Walbot V

COMMENT
CONTACT: MAIBOL V
Department of Biological Sciences

Department of Biological Sciences
Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

plate: 614068 row: G column: 07.

FEATURES

Location/Qualifiers

QY	562	GTCAATGATTTTGGTGAAACAGATGTTGAGTGATATCCATTGAAGTTCCTGGTGAAGAACCA	621
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QY	682	TTATCCACCAAGGTGAAATACGCTTGCAGAAAGCTGAGCAGGTGACATGCACACCCCTG	741
DB	421	TTATCCACCAAGGTGAAATACGCTTGCAGAAAGCTGAGCAGGTGACATGCACACCCCTG	480
QY	742	GATTATAGTGAAGACCAAGACCTGTTCCCGAGAGATAAGCAGCCAGCTGAAACAGCC	801
DB	481	GATTATAGTGAAGACCAAGACCTGTTCCCGAGAGATAAGCAGCCAGCTGAAACAGCC	540
QY	802	CCAAGACCTTCATACCATCTTCAAGGCGAAGAAAGACTGGGATAAACTGGAAGCTGAA	861
DB	541	CCAAGACCTTCATACCATCTTCAAGGCGAAGAAAGACTGGGATAAACTGGAAGCTGAA	600
QY	862	GTCAAAAAGGAGGAGAGGAAG	883
DB	601	GTCAAAAAGGAGGAGAGGAAG	622
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DEFINITION	614028B03.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA, mRNA sequence.		
ACCESSION	AW042392		
VERSION	AW042392.1	GI:5901292	
KEYWORDS	EST.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Maize ESTs from various cDNA libraries sequenced at Stanford University		
AUTHORS	Contact: Walbot V		
TITLE	Department of Biological Sciences		
JOURNAL	Stanford University, Palo Alto, CA 94304, USA		
COMMENT	855 California Ave, Palo Alto, CA 94304, USA		
	Tel: 650 723 2227		
	Fax: 650 725 8221		
	Email: walbot@stanford.edu		
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Best Local Similarity	99.7%	Pred. No. 2.6e-152;	
Matches 584; Conservative	0; Mismatches 2; Indels 0; Gaps 0;		
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QY	267	TGCAAGGCTGCTCTTGAAGTGGGTTCTTCTTATGATCAGGCGATTCAAGGTTGCTCG	326
DB	121	TGCAAGGCTGCTCTTGAAGTGGGTTCTTCTTATGATCAGGCGATTCAAGGTTGCTCG	180
QY	327	TCATTATGAAGGAATGTGATGAGCGCATCGCTGAGGAATCTAGCCAGGCACAGTAAAGAA	385
DB	181	TCATTATGAAGGAATGTGATGAGCGCATCGCTGAGGAATCTAGCCAGGCACAGTAAAGAA	240
QY	387	TGTTGAGGCTACTGTGGCTGCTACTATTGAGGACAAAGGAGATTCAAAATATGAGAA	446
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QY	447	TACACACACAGTATAGAACCCCGCAGCAAAACCAAAATACAGGATGACTTACCAACAG	506
DB	301	TACACACACAGTATAGAACCCCGCAGCAAAACCAAAATACAGGATGACTTACCAACAG	360
QY	507	TGCCACAGAAAGTGGTACTGACCAATATTGCTAAGGGTGTTCCTGCTGATGATGATCAT	566
DB	361	TGCCACAGAAAGTGGTACTGACCAATATTGCTAAGGGTGTTCCTGCTGATGATGATCAT	420
QY	567	TGATTTTGGTGAAACAGATGTTGAGTGATATCCATTGAAGTTCCTGGTGAAGAACCATACCA	626
DB	421	TGATTTTGGTGAAACAGATGTTGAGTGATATCCATTGAAGTTCCTGGTGAAGAACCATACCA	480
QY	627	TTTTGAGCCCGCTGCTGTTTCTTAAGATTTATCCCTGAGAAATGCAAAATATCAAGCTTATC	686
DB	481	TTTTGAGCCCGCTGCTGTTTCTTAAGATTTATCCCTGAGAAATGCAAAATATCAAGCTTATC	540
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DB	541	CACCAAGGTTGAAATACGCTTGCAGAAAGCTGAGCAGGTGACATGG	586
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DEFINITION	SCAGFL3023C08.g Saccharum officinarum FL3 Saccharum officinarum cDNA clone SCAGFL3023C08 5', mRNA sequence.		
ACCESSION	CA229238		
VERSION	CA229238.1	GI:35291554	
KEYWORDS	EST.		
SOURCE	Saccharum officinarum		
ORGANISM	Saccharum officinarum		
REFERENCE	1. (bases 1 to 609)		
AUTHORS	Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.		
TITLE	The libraries that made SUCEST		
JOURNAL	Genet. Mol. Biol. 24 (1-4), 1-7 (2001)		
COMMENT	Contact: Arruda P		
	Centro de Biologia Molecular e Engenhariaia Genetica		
	Universidade Estadual de Campinas		
	Caixa Postal 6010, 13083-970, Campinas SP, Brazil		
	Tel: 55 19 3788 1137		
	Fax: 55 19 3788 1089		
	Email: parruda@unicamp.br		
	Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bccc.unesp.br		
	Plate: 023 row: C column: 08		
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source	1..609		
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
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(without alignments)
10590.311 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gsl1:*
- 9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1378.2	94.7	1646	3	AY103953	Zea mays
2	719	49.4	727	6	CA401716	EL01N0424
3	708.2	48.7	752	6	CD443320	EL01N0424
4	699	48.0	1131	9	CL959360	OBIFCC002
5	660.6	45.4	686	6	CF041238	OCI23F02
6	657.2	45.2	772	6	CA258233	SCCCT300
7	652.4	44.8	668	2	AW076274	614063D11
8	650.8	44.7	798	6	CA176210	SCJLST102
9	647	44.5	756	6	CA184150	SCRFST314
10	643.4	44.2	659	2	AW090936	614068G07
11	641	44.1	759	6	CA245820	SCEZFL508
12	637.4	43.8	778	6	CA227695	SCJLFL301
13	631	43.4	666	6	CA215140	SCSBAD112
14	628.8	43.2	681	2	AW076372	614066C10
15	627	43.1	658	2	AW155786	614096F11
16	623.2	42.8	648	1	AI603781	486096G09
17	615.4	42.3	665	6	CA153735	SCVPRZ203
18	608.2	41.8	678	6	CA177070	SCWCST105
19	601.8	41.4	725	6	CA094787	SCCCL401
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23	596.4	41.0	622	6	CA229980	SCJFL3C0
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26	591	40.6	591	2	AW018202	AW018202
27	589.8	40.5	593	4	BG265701	BG265701
28	584.4	40.2	594	1	AI601072	AI601072
29	583.4	40.1	586	2	AW042392	AW042392
30	583.4	40.1	609	6	CA229238	SCAGFL302
31	579.8	39.8	718	6	CA106435	SCQHR101
32	576.8	39.6	702	6	CA282995	SCPRLB202
33	576	39.6	588	5	BU499669	946178B11
34	571.2	39.3	680	6	CA128103	CA128103
35	567.8	39.0	578	2	AW000264	AW000264
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37	563	38.7	574	4	BI644145	BI644145
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40	558.4	38.4	607	1	AI601071	AI601071
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ALIGNMENTS

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DEFINITION Zea mays PC0098564 mRNA sequence.
ACCESSION AY103953
VERSION AY103953.1 GI:21207031
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1646)
AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M., Tingey, S.V.
TITLE Zea Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1646)
AUTHORS Coe, E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA

Comment: If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

Location/Qualifiers
1..1646
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/clone_lib="Maize Mapping Project/DuPont Consensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN
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[illegible]

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Db	1343	GTCACCCATAGTCCCATGAGCTTGCTTGGTTAAGTCTCTGCTTTGTAAAGCTTTCTGTA	1402
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Db	1403	TGACAGTCTAGCGTGTCTCTGAGTGTACTTTCGCGTAGCTTTTGATGGACATAGGATGC	1462
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RESULT 2			
CA401716/c			
LOCUS	CA401716	727 bp	mRNA linear EST 07-NOV-2002
DEFINITION	EU010424G10.g EndospERM_4 Zea mays cDNA, mRNA sequence.		
ACCESSION	CA401716		
VERSION	CA401716.1	GI:24766567	
KEYWORDS	EST.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	Lai, J., Dev, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F., Larkins, B., Becraft, P. and Messing, J.		
TITLE	Characterization of the maize endospERM transcriptome and its comparison to the rice genome		
JOURNAL	Genome Res. 14 (10), 1932-1937 (2004)		
COMMENT	Contact: Lai, Jinsheng Dr. Joachim Messing's lab Waksman Institute, Rutgers University 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA Tel: 732-445-3801 Fax: 732-445-5735 Email: jlai@waksman.rutgers.edu Seq primer: T7		
FEATURES	Location/Qualifiers		
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	/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"		

[illegible]

u8-10-609-078-7.rst

Email: jlai@waksman.rutgers.edu
Seq primer: T3.
Location/Qualifiers
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XhoI"

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QY	718	CGT	CTGTTTTCTAAGATTATCCCTGAGAAATGCAATATCAAGTCTTATCCACCAAGGTT	777
Db	254	CGT	CTGTTTTCTAAGATTATCCCTGAGAAATGCAATATCAAGTCTTATCCACCAAGGTC	313
QY	778	GAA	ATACGGCTTGC AAAAGCTGAGCAGGTGATCGGACAAACCTTGGATTATAGTGGGAAGA	837
Db	314	GAA	ATACGGCTTGC AAAAGCTGAGCAGGTGATCGGACAAACCTTGGATTATAGTGGGAAGA	373
QY	838	CAA	AGACTGTTCCCGCAGNATAGCAGCGCCAGCTGAAACAGAGCCCAAGACCTTTCATAC	897
Db	374	CAA	AGACTGTTCCCGCAGNATAGCAGCGCCAGCTGAAACAGAGCCCAAGACCTTTCATAC	433
QY	898	CCAT	CTTCAAAGCGCAAAAAGACCTGGGATAAATCTGGAACTGAAGTCAAAAAGGAGGAG	957
Db	434	CCAT	CTTCAAAGCGCAAAAAGACCTGGGATAAATCTGGAACTGAAGTCAAAAAGGAGGAG	493
QY	958	AAG	GAAGAAAACCTTGATCGGTGATGCTGCATTGAAACAAATTCCTCCGTGACATCTACAAG	1017
Db	494	AAG	GAAGAAAACCTTGATCGGTGATGCTGCATTGAAACAAATTCCTCCGTGACATCTACAAG	553
QY	1018	GAT	GCTGATGAAGATATCGGAGGGCCATGATGAAGTCAATTCGTGGAAATCAATGGCACT	1077
Db	554	GAT	GCTGATGAAGATATCGGAGGGCCATGATGAAGTCAATTCGTGGAAATCAATGGCACT	613
QY	1078	GTT	CTCTCAACCAATTTGGAAAGATGTTGGAGCAAGAAAGGTAGAAGGGAGCCCC	1131
Db	614	GTT	CTCTCAACCAATTTGGAAAGATGTTGGAGCAAGAAAGGTAGAAGGGAGCCCC	667

RESULT 8
 CAI76210/c
 LOCUS
 DEFINITION
 CAI76210
 798 bp mRNA linear EST 24-SEP-2003
 SCULST1027D01.b ST1 Saccharum officinarum cDNA clone SCULST1027D01
 3', mRNA sequence.
 CAI76210
 CAI76210.1 GI:35105709
 EST.
 Saccharum officinarum
 Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
 complex.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1. (bases 1 to 798)
Vettores, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
<http://www.bccccenter.fcav.unesp.br>
Plate: 027 row: D column: 01
1. year. 506 Promoter primer.

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 Db 629 TAAGGCGTTCTCGCTGATAGTGTAGTCATTGTTGGTGAACAGATGTTTAAGTGTATC 688
 Qy 678 CATTGAAGTTCTCGGTGAAGACCATACCATTTTCAGCCCCCGTCTGTTTTCTAAGATTAT 737
 Db 689 CATTGAAGTTCTCGGTGAAGACCATACCATTTTCAGCCCCCGTCTGTTTTCTAAGATTAT 748
 Qy 738 CCCTGAGAAATGCAAATATCAAGT 761
 Db 749 CCCTGAGAAATGCAAATATCAAGT 772

RESULT_7	
AW076274	
LOCUS	
DEFINITION	614063D11.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA,
	668 bp mRNA linear EST 14-OCT-1999
ACCESSION	AW076274
VERSION	AW076274.1
KEYWORDS	mRNA sequence.
SOURCE	EST.
	Zea mays
ORGANISM	Zea mays
PREFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 668)

Walbot V.	Maize ESTs from various cDNA libraries sequenced at Stanford
University	
Unpublished (1999)	
Contact: Walbot V	
Department of Biological Sciences	
Stanford University	
855 California Ave,	Stanford, CA 94304, USA
Tel: 650 723 2327	
Fax: 650 725 8221	
Email: walbot@stanford.edu	
Plate: 614063	row: D, column: 11.

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FEATURES
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Query Match	44.8%;	Score 652.4;	DB 2;	Length 668;
Best Local Similarity	99.8%;	pred. No. 3.6e-158;		
Matches 653;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0
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QY	538	GTGTATAGAACCCCAAGCAACCAAAATACAGGCGATGACTACTACAACAGTGGCCACAGAA	597	
Db	74	GTGTATAGAACCCCAAGCAACCAAAATACAGGCGATGACTACTACAACAGTGGCCACAGAA	133	
QY	598	GTGTGTACTGCACAATAATTTGCTAAAGGGTTCCTCTGATAGTGTAGTCATTGATTTTGGT	657	
Db	134	GTGTGTACTGCACAATAATTTGCTAAAGGGTTCCTCTGATAGTGTAGTCATTGATTTTGGT	193	

QY 385 TCAGGCGATTCAAGGTTTCTGCTCTATTGAGGAATGTGATGAGCCATCGCTGAGGAA 444
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 Db 361 TCTAGCCAGCACCAGTAAGAGATGTTGAGGCTACTGCTGCTCTATTGAGGACAAG 420
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 Db 601 GTTCCTGCTGATGAGAACCATACCATTTTCAGCCCGCTGTTTCTAAGATTTATCCCTGAG 660
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 QY 805 GTGACATGGACACCCCTGGATATTAGTGGAGAACCAAG 843
 Db 718 GTGACATGGACACCCCTGGATATTAGTGGAGAACCAAG 755

RESULT 10
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 LOCUS 614086G07.y1.614 - root cDNA library from Walbot Lab Zea mays cDNA,
 DEFINITION mRNA sequence.

ACCESSION
 VERSION AW090936
 KEYWORDS EST.

SOURCE
 ORGANISM Zea mays

REFERENCE
 AUTHORS Zea mays
 TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 659)

Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished (1999)
 Contact: Walbot V

Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 614068 row: G column: 07.

FEATURES
 source

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 Lab (LM)"

ORIGIN

Query Match 44.2%; Score 643.4; DB 2; Length 659;
 Best Local Similarity 99.8%; Pred. No. 7,9e-156;
 Matches 644; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 75 TCATCAGGCGATTCAAGGTTTCTGCTCTATTGAGGAATGTGATGAGCGATCCCTGA 134
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 Db 135 GGAATCTAGCCAGGCAACCAAGTAAAGATGTTGAGGCTACTGTGGCTGCTACTATTGAGGA 194
 QY 501 CAAGGAGGATTTCAAAATATGAGAAATACACCAAGTGTGATAGAACCCCAAGCAAAACC 560
 Db 195 CAAGGAGGATTTCAAAATATGAGAAATACACCAAGTGTGATAGAACCCCAAGCAAAACC 254
 QY 561 AAAATACAGGCACTACTACTACCAAGTGTGATAGAACCCCAAGTGTGATAGAACCCCAAGCAAAACC 620
 Db 255 AAAATACAGGCACTACTACTACCAAGTGTGATAGAACCCCAAGTGTGATAGAACCCCAAGCAAAACC 314
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 QY 681 TGAAGTCTGCTGATAGAACCAATACATTTTCAAGCCCGCTGTTTCTAAGATTTATCCC 740
 Db 375 TGAAGTCTGCTGATAGAACCAATACATTTTCAAGCCCGCTGTTTCTAAGATTTATCCC 434
 QY 741 TGAGAAATGCAATATCAAGTCTTATCCACCAAGTGTGAAATACGCTTGCAGAAAGCTGA 800
 Db 435 TGAGAAATGCAATATCAAGTCTTATCCACCAAGTGTGAAATACGCTTGCAGAAAGCTGA 494
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 Db 495 GCAGGTGATGATGCAACCCCTGGATATTAGTGGAGAGACCAAGACTGTTTCCCAAGAAAT 554
 QY 861 AAGCAGCCAGCTGAAACAGCCCAAGACCTTTCATACCCATCTTCAAGGCGGCAAAAGA 920
 Db 555 AAGCAGCCAGCTGAAACAGCCCAAGACCTTTCATACCCATCTTCAAGGCGGCAAAAGA 614
 QY 921 CTGGGATTAACCTGGAGGCTGAAGTCAAAAGGAGAGAGGAAGA 965
 Db 615 CTGGGATTAACCTGGAGGCTGAAGTCAAAAGGAGAGGAAGA 659

RESULT 11

CA245820 759 bp mRNA linear EST 25-SEP-2003
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 DEFINITION cDNA clone SCEZFJ5084D06 5', mRNA sequence.

ACCESSION
 VERSION CA245820
 KEYWORDS EST.

SOURCE
 ORGANISM Saccharum officinarum

REFERENCE
 AUTHORS Vettore,A.L., da Silva,F.R., Kemper,B.L. and Arruda,P.
 TITLE The libraries that made SUCST
 JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 COMMENT Contact: Arruda P.
 Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil

735 TATCCTCGAGAAATGCAAAATATCAAGCTCTTATCCACCAAGGTTGAAATATCGCCTTCGAAA 794
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